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Carson,D.A.
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order(L42627.1:1. .199,L42628.1:1. .316,L42629.1:1. .190,
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L42632.1:64. .303,L42633.1:76. .198,138. .176)
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/chromosome="9"
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Carson,D.A. and Carrera,C.J.
Method for suppressing multiple drug re
Patent: US 6210917-A 1 03-APR-2001;
Location/Qualifiers
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LILGKIKNVDCVLLARHGRQHTIMPSKVNYQANIWALKEEGCTHVIVTTACGSLREEI
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QPGDIVIIDQFIDRTTMRPQSFYDGSHSCARGVCHIPMAEPFCPKTREVLIETAKKLG
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/mol_type="unassign
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1 (bases 1 to 2763)

Carrera, C.J., Carson, D.A., Cottam, H.B. and Nobori, T.

Method for inhibiting adenylosuccinate synthetase activity

methylthicadenosine phosphorylase deficient cells

Patent: US 5840505-A 1 24-NOV-1998;

Location/Qualifiers

1. 2763

1. 2763
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AR342446
AR342446.1
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Carson,D.A., Schmid,M. and Carrera,C.J.
Method for early diagnosis of, and determination
cancer
Patent: US 6576420-A 25 10-JUN-2003;
Location/Qualifiers
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Location/Qualifiers
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/mol_type="genomic
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Laird,G.

Direct Submission

L Submitted (17-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Jan 13, 2001 this sequence version replaced gi:11878000.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. The following abbreviations are used to associate primary accession
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irson, D.A. and Nobori, T.
/clin dependent kinase 4 inhibitor
atent: US 6689864-A 14 10-FEB-2004;
Location/Qualifiers
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malia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 168656)
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Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Informat
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequent
was generated from part of bacterial clone contigs of human
chromosome 9, constructed by the Sanger Centre Chromosome 9 Magroup. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr9
RP11-70L8 is from the library RPCI-11.1 constructed by the graphic de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
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2 (bases 1 to 250000)

Yokota,J., Kohno,T., Inou
Direct Submission
Submitted (25-APR-2001)
Research Institute, Biolo
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                                                                                                                                                              Eukaryota;
Mammalia; E
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                                                                                  Kohno, T., Inoue, K., Kitagawa, Y., Hayas
Mizoguchi, H. and Yokota, J.
Prevalent Involvement of Illegitimate
Chromosome 9p21 Deletions in Lymphoid
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/note="Single clone region. As restriction digest data."
157251...157348
/note="Single clone region. Legion of the clone region. Legion restriction digest data"
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/chromosome="9"
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Institute,
                                                                                                                                                               Eutheria;
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                                           Inoue, K.
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5/CDKN2A,
  Division;
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              Kohno,
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            Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
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Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
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Guerra,W., Guevara,W.,
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Guerra,W., Guevara,W.,
Guerra,W., Guerra,W., Guevara,W.,
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/gene="p16/CDKN2A"
complement(join(185617. .1
192072. .192221))
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                                                                                                                                                                                                                                                                                                                                                                                                                                            .5 GI:25006711
S_PHASE1; HTGS_DRAFT; H
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MEPAAGSSMEPSADWLATAAARGRVEEVRALLEAGALPNAPNSYGRRPIQVMMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD"
                                                                                                                                                                                                                                                                                                                                                                                          ; Metazoa;
Eutheria;
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/chromosome="9"
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Havlak,P.,
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Hawes, A.,
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 Henderson, N.,
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    Hernandez, J.
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                                        Guevara, W.
                                                                           Foster, P.,
                                                                                                                    Eaves, K.,
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Hernandez, R., Hines, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Kahan, Z., King, L., Kovar, C., Kowis, C., Kiu, Y., Lubow, H., Levan, J., Lewis, L., Li, Z., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuhewa, L., Loulseged, H., Lozado, R.J., Lu, X., Ma, J., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mangum, A., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Maheshwari, M., Morris, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankery, S., C., Neal, D., Newton, N., Yguyen, N., Norris, S., Nankery, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Plage, F., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rokley, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Snedd, A., Solergren, E., Song, M., Rose, R., Ruiz, S.J., Steimle, M., Strong, R., Sutton, A., Syatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Vallasana, D., Waldron, H., Walker, B., Wang, J., Warren, R., Wells, A., Tabor, P., Taylor, C., Wallson, R., Wleczyk, R., Woden, H., Worley, K., Warght, D., Walson, J., Zhou, J., Zhou, J., Zhou, J., Zhou, J., Zhou, J., Zhou, S., Dunn, D., von, V., Yu, F., Zhang, J., Walse, R., Smith, D.R., Holt, R.A., Smith, H.O., Meinstock, G., and Glbbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of Molecular and Human Genetics, Baylor College of Medicine, One Baylor plaza, Houston, TX 77030, USA
On Nov 15, 2002 this sequence version replaced gi:23101222.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
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Direct Submission
Submitted (05-FEB-2002) Human Genome Sequencing Cerof Molecular and Human Genetics, Baylor College of Baylor Plaza, Houston, TX 77030, USA

'dases 1 to 225782)

Consortium.
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Center project name: GPKA
Center clone name: CH230-276K5
Assembly program: Phrap; version 0.990329
Consensus quality: 180465 bases at least Q40
Consensus quality: 184814 bases at least Q30
Consensus quality: 187892 bases at least Q20
Estimated insert size: 188688; sum-of-contigs estimation
Estimated insert size: 188688; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Baylor College of Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
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REFERENCE AUTHORS TITLE

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RESULT 11
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                                                                                                                                                                                                                                                                                          HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
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AC108638
Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
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213124
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224103
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larity 87.5%;
Conservative
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/note="wgs_contig"

145017. .147149

/note="wgs_contig"

221119. .222830
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1. .225782
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222881. .224002
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'clone="CH230-276K5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="wgs_contig"
11156. .112668
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Pred. No. 4.8e-07;
); Mismatches 10
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Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Ferrandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garne, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Guratuke, P., Haalland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hogues, M., Hollins, B., Howells, S., Hlayk, S., Hune, J., Idlebird, D., Jackson, A., Hollins, B., Howells, S., Hlyk, S., Hune, J., Idlebird, D., Jackson, A., Hollins, B., Howells, S., Hulyk, S., Kan, Z., King, L., Kovar, C., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lobow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Louiseged, H., Lozado, R.J., Iu, X., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martin, R., Martinez, E., Mensen, E., Morgan, M., Morris, K., Morris, S., Menen, E., Menen, E., Morgan, M., Morris, K., Morris, S., Munidasa, M., Nurphy, M., Nair, L., Nair, J., Nair, J., Liu, Z., Liu, J., Lorensubewa, L., Colarpunsagoon, A., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, S., Parks, K., Morris, S., Morris, S., Morens, S., Pu, L.-L., Mankervis, C., Real, D., Newton, N., Nguyen, N., Norris, S., Nair, J., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Shatsman, S., Shen, H., Shetty, J., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Sanders, M., Sutcon, A., Satek, A., Tabor, P., Taylor, C., Shetty, J., Shen, H., Shen, H., Shen, H., Walley, R., Hilly, M., Reilly, M., Reilly
                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission

L Submitted (08-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Sep 23, 2002 this sequence version replaced gi:21737759.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome sequence and whole genome shotgun sequence reads. Both end sequences and whole genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Worley, K.C.
Direct Submission

Submitted (31-JAN-2002) Human Genome Sequencing Center, Department Submitted (31-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 287775)
                                                                                                                                                                                                                                                                                                                                            shotgun
table.
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Web site: http://www.hgsc.bcm.tmc.Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GPRQ
Center clone name: CH230-46K10
                                                                                                                                                                                                                   Center
                                                                                                                                                                                                                                                        Center:
                                                                                                                                                                                                                                                                                                                                                                                    sequence
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JOURNAL REFERENCE

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DEFINITION
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                                                                                                                                                                                                                                                                                              RESULT 12
AR425810
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Best Local
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AR425810
AR425810.1
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                                               1 (bases 1 to 499)
Edwards, J.-B.D.M., Jobert, S. and Giordano, J.-Y
EST's and encoded human proteins
Patent: US 6639063-A 17307 28-OCT-2003;
Location/Qualifiers
                                                                                                                                                Unknown.
Unclassified.
                                                                                                                                                                                                                                                                                 AR425810
                                                                                                                                                                                      Unknown.
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NOTE: This sequence may represent more than one clone.
NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                             ATTAAAACAGCATGGCTGAC
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64031
117548
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Consensus quality: 238829 bases at least Q40
Consensus quality: 241996 bases at least Q30
Consensus quality: 244256 bases at least Q20
Estimated insert size: 269456; sum-of-contigs estimation
Quality coverage: 4x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGAC
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3931 64030: gap of unknown length
4031 117547: contig of 53517 bp in length
7548 117647: gap of unknown length
7648 248038: contig of 130391 bp in length
8039 248138: gap of unknown length
8139 249750: contig of 1612 bp in length
9751 249850: gap of unknown length
9851 278054: contig of 28204 bp in length
8055 278154: gap of unknown length
8155 283612: contig of 5458 bp in length
3613 283712: gap of unknown length
3713 287775: contig of 4063 bp in length
Location/Qualifiers
1. .287775
                                                                                                                                                                                                                                                                17307
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-46K10"
                   organism="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="wgs_contig"
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type="genomic
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                                                                  Eukaryota; Metazoa; Chordata; C
Mammalia; Eutheria; Primates; C
1 (bases 1 to 499)
Edwards, J.B.D.M., Jobert, S. and
EST and encoded human protein
Patent: JP 2002010789-A 13440 1
GENSET CORP
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EST and encoded human pro
BD121363
BD121363.1 GI:23216273
JP 2002010789-A/13440.
Homo sapiens (human)
Homo sapiens
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Sequence 17
AX986504
AX986504.1
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                         sh 42.7%;
Similarity 89.0%;
65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     th 42.7%; Similarity 89.0%; 65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              Dumas Milne Edwards, J.B., Jobert, S. and ESTs and encoded human proteins Patent: EP 1104808-A 17307 06-JUN-2001; Genset (FR)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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Nobori, T., Takabayashi, K., Tran, P., Orvis, L., Batova, A., Yu, A.L.
and Carson, D.A.
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Direct Submission
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Research on Aging, and Department of Medicine, University
California at San Diego, La Jolla, CA 92093-0663, USA
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Genomic cloning of methylthioadenosine phosphorylase: a purine metabolic enzyme deficient in multiple different cancers Proc. Natl. Acad. Sci. U.S.A. 93 (12), 6203-6208 (1996) 96234115 8650244 [1986]
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                                                                                                                                        This is the DNA sequence of a human methylthioadenosine phosphorylase C (MTAse) genomic DNA clone that was isolated from a cosmid gene library using an MTAse cDNA probe. The encoded enzyme catabolises methylthioadenosine to adenine for endogenous salvage incorporation into the intracellular AMP pool. The invention relates to methods for treating and preventing the onset and maintenance of multiple drug resistance (MDR) in animals undergoing cancer chemotherapy. In the methods provided, cells are depleted of AMP and ATP and are thus unable to supprt P-C glycoprotein activity. One method obtains a population of target cells are treated with a purine synthesis inhibitor, such as L-alanosine, which starves the cells of adenine and suppresses P-glycoprotein activity. The Starves the cells of adenine and suppresses P-glycoprotein activity. The small-cell lung cancer cells, acute lymphoblastic leukemia cells comprising cells or urothelial tumor cells, preferably primary tumour cells comprising cells are also treated for MDR with purine synthesis inhibitors. MTAse competent and deficient cells are also treated for malignancy with other canti-cancer drugs. MTase sequence-specific oligonucleotides can be used to detect the presence or absence of MTAse in malignant cell lines
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02-JUN-1995;
04-MAY-1998;
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                                                                                                                                           interferon-alpha; CDK4I; tumour suppressor; chromosome-9p21; cyclin-dependent kinase-4-inhibitor; probe; primer; mutation; melanoma; diagnostic; dysplastic nevus syndrome; glioma; non-small cell lung carcinoma; cancer; gene therapy; antisens, antibody; imaging; ss.
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useful
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Similarity 99.3%;
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                   Methylthioadenosine phosphorylase; MTAse; adenylsuccinate synthetase; lung cancer; acute lymphoblastic leukaemia; urothelial
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                                                                                                                                                                                                                                                              Claim
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This DNA sequence comprises human genomic DNA for methylthioadenosine phosphorylase (MTase), obtained from a cosmid gene library constructed from human placenta DNA by screening with a MTase cDNA probe. A claimed method for inhibiting the activity adenylsuccinate synthetase (ASS) in mammalian cells deficient in MTAse activity involves: (a) determining that a population of cells obtained from a mammalian host is MTase deficient; and (b) administering an ASS inhibitor (preferably L-C depleted of AMP. The method is especially used to treat human MTAse-C deficient primary tumour cells, specifically non-small cell lung cancer, acute lymphoblastic leukaemia (ALL), glioma and urothelial tumour cells. MTAse catabolises methylthioadenosine to adenine for endogenous salvage in selective killing of substrate for de novo synthesis of AMP, resulting coligonuclotides can be used to detect the presence or absence of MTAse in malignant cell lines
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This invention describes a novel method for detecting catalytically active and inactive methylthioadenosine phosphorylase (MTAse) in mammalian cells, using oligonucleotide probes which hybridize to MTAse nucleic acid coding regions. Detection of MTAse encoding nucleic acid indicates the cell has catalytically active MTAse. The method is useful for detecting malignant cells with a deficient MTAse gene, useful for identifying malignant cells which are suitable targets for methionine (MET) starvation therapy. The new method is simple, efficient and successful at determining MTAse negative cells, unlike prior art cultures, which include analysis of catalytic activity in cell cultures, requiring a commercially unavailable radiochemical substrate, and immunoassays, using MTAse antibodies which are unable to be produced in sufficient quantities. Recombinant MTAse protein produced using the new polynucleotide and vector, allows greater and purer production of
                                                                                                                                                                               Detecting catalytically active and inactive methylthicadenosine phosphorylase (MTAse) in mammalian cells useful for identifying recells which are suitable targets for methionine (MET) starvation
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                                                                                                                                                                                                   resent invention relates to inhibiting adenyl succinate synthetase activity in methylthioadenosine phosphorylase (MTAse) deficient of mammalian host. The invention may be used as a treatment for r, especially breest and colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J
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TCAAAATCTGGTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATAT
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larity 99.3%;
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Pred. No. 1.2e-30;
0; Mismatches 1;
                                                                            Score 139.4; DB 5
Pred. No. 1.2e-30;
0; Mismatches 1
                                                                                                                                                             C; 598 G;
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                                                        The present invention relates to novel tumour suppressor genes, termed as cyclin-dependent kinase 4 inhibitor (CDK4I) genes and their corresponding proteins. The polynucleotides are useful for preparing a composition for diagnosing or treating cancer. Sequences of the invention are also useful in gene therapy. The present sequence is human methylthicadenosine phosphorylase (MTAse) genomic DNA used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                     exon
                                                                                                                                                                                                                                                                                                                                                                            Human;
CDK4I;
                                                                                                                                                       WPI;
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                                          Sequence
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AATCAAAATCTGGTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATAT
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              98.9%;
larity 99.3%;
Conservative
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gene therapy; methylthioadenosine
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                                                                                                                                                                                     Antigenic peptides may be generated from this sequence encoding methyladenosine-phosphorylase, which are then used to generate antibodies specific for MTAse. The produced antibodies may be used in an immunoassay for the detection of MTase
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                                                                                                                                                                                                                                          Disclosure
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                                                                                                                                                                   84 BP; 781 A; 505 C; 598 G; 804 T; 0 U; 96 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAGTAGCATGGCTGCCCAG 2328
                                                                                                                         98.9%; Score 139.4; DB 2
larity 99.3%; Pred. No. 1.2e-30;
Conservative 0; Mismatches 1
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                                                                                                                                                                                                                                        Page 27-28; 46pp; English.
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RESULT 10
ABQ59540/c
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ABQ59540;
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AC
ABQ59540;
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Human; color
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Homo sapic
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                                                                                                                                                                                                                                                                                                                             ABQ56306 to ABQ60787 represent isolated nucleic acids (I) differentially expressed in cancer tissues. ABB78993 to ABB79004 represent proteins cencoded by the ABQ60776 to ABQ60787 nucleic acid sequences. (I) can be used in antisense therapy. An antibody immunoreactive with a polypeptide cencoded by (I) is useful for detecting cancer in a patient sample, and concleic acid which hybridises to (I) in a cell. A probe/primer derived from (I) can be used for determining the presence of a nucleic acid which hybridises to (I) in a cell. A probe/primer derived of cells from a patient. (I) is useful for determining the phenotype of cells in a sample concerning the patient of cells in a sample concerning the patient. (I) is useful for determining the presence of cancer in a cell or tissue type, for determining the presence or state of other type of cancer, in antisense therapy, to generate macroarrays on a solid surface, to identify a chromosome on which the corresponding gene resides, and in tissue profiling, forensics, genetic analysis, mapping and diagnostic applications. (I) can be used to raise antibodies, and to screen for peptide analogues and antagonists
                                                                                                                                                                                        Query Match
Best Local S
Matches 63
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Thiaglingam
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380
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Similarity 96.9%;
63; Conservative
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canalysis; diagnostic;
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Pred. No. 3.2e-08;
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RESULT 11 AAH33683 ID AAH3

**AAH33683** 

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                                                                                                                                                                                                          Query Match
Best Local S
Matches 69
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useful f
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P-PSDB; AAG74252
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65; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acids encoding 4277 human colon cancer-associated polypeptides, for preventing, diagnosing and/or treating colorectal cancers.
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                                                                                                                                                        21 and 7922
                                                                                                                              TGGCTGCCCAG 141
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larity 89.0%;
Conservative
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99US-0163280P.
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                                                                                                                                                                                                                                  Length 1437;
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cc invention also relates to nucleic acid sequences (ADC29919-CC invention also relates to nucleic acid sequences (ADC39919-ADC31860). The creation also relates to nucleic acid sequences over 99% identical with the novel human cDNAs. The invention additionally encompasses expression vectors and host cells comprising a nucleic acid of the invention; the recombinant production of a polypeptide of the invention; an antibody compound which binds to a polypeptide of the invention; and methods of identifying a compound which binds to a polypeptide of the invention. The cinvention further discloses methods of polypeptide of the invention; and methods of invention further discloses methods of polypeptide of the invention. The conting sequences corresponding to the cDNA sequences of the invention of conting sequences corresponding to the cDNA sequences of the invention are useful in diagnostics, drug screening, forensics, gene mapping, in the cidatification of mutations responsible for genetic discreters of the also used for treating biodiversity, and in producing many other types of discase and other neurodegenerative diseases, anaemia, platelet cidscorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or comprisers, and in the recombinant production of a portein. The polypeptides are also useful in generating antibodies, as molecular weight markers, and as food supplements. The present sequence represents a specifically claimed human cDNA sequence of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was contained in electronic format directly from WIPO at the sequence data for the supplements. The present sequence represents a specifically obtained in electronic format directly from WIPO at
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Haley-Vicente D,
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P-PSDB; ADC31298.
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Asundi V,
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's disease;
a; platelet
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Sequence

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Best Local S
Matches 65
                                     This invention relates to novel combination therapies that selectively kill methylthioadenosine phosphorylase (MTAP) deficient cells. The combination therapies comprise administering an inhibitor of glycinamide ribonucleotide formyltransferase (GARFT) and/or aminoimidazolecarboximide ribonucleotide formyltransferase (AICARFT), and administering an anticombination therapies can be used for selectively killing MTAP deficient cells, and for treating cell proliferative disorders e.g. lung cancer, leukaemia, glioma, urothelial cancer, colon cancer, breast cancer, prostate cancer, pancreatic cancer skin cancer and head and neck cancer. The anti-toxicity agent counteracts the toxicity of the inhibitor in the MTAP-competent (i.e. healthy) cells and increases the maximally tolerated dose of the inhibitor. This polynucleotide sequence represents the cloned when the invention
                                                                                                                                                                                                                                                                                                                                                                                 Bloom LA,
Zehnder L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        combination therapy; methylthicadenosine phosphorylase; MTAP; inhibitor; glycinamide ribonucleotide formyltransferase; GARFT; aminoimidazolecarboximide ribonucleotide formyltransferase; AICARFT; anti-toxicity agent; cell proliferative disorder; lung cancer; leukaemia glioma; urothelial cancer; colon cancer; breast cancer; prostate cancer; pancreatic cancer; skin cancer; head; neck cancer; gene; ss.
                                                                                                                                                                                                                                                                                    used for transleglycinamide
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09-DEC-2002;
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                             of
                                                                                                                                                                                                                                                                                       y killing methylthioadenosine phosphorylase deficient cells reating cell proliferative disorders comprises administering e ribonucleotide formyltransferase and anti-toxicity agent.
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2002US-0432275P.
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89.0%;
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Meng JJ;
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Pred. No. 1.2e-07;
D; Mismatches 8
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                                                                                          The present sequence is one of a large number of 5' ESTs derived from C mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from C total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA C libraries. Such ESTs are not well suited for isolating cDNA sequences are derived from mRNAs and even in those cases where longer C cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in C diagnostic, forensic, gene therapy and chromosome mapping procedures. C expression and secretion vectors
                                     Query Match
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Matches 49
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Matches
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ilarity 98.0%;
Conservative
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Pred. No. 0.00
O; Mismatches
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17-OCT-2001;
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variation
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single
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                                                                                                                                                                                                                                                                              lated nucleic acid comprising allelic variant of polymorphic thrombospondin 1 or 4 gene, useful for identifying ition of subject to develop vascular disease associated with
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                                                                                                                                   thrombospondin 1 (THBS1) or THBS4 genes. The invention also nucleic acid comprising allelic variant of polymorphic region r THBS4 gene. The method is useful for identifying a subject as e for a particular clinical course of therapy or to treat a isease or disorder and for selecting a clinical course of treat a subject who is at risk for developing a vascular disorder. The present sequence is human THBS4 reference gene. sequence is said to encode SEQ ID NO: 4 (AAE36229). However not appear to be the case
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                                                                           27.1%;
nilarity 58.3%;
Conservative
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leotide polymo:
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ALIGNMENTS

## RESULT 1 US-08-956-657-1 ; Sequence 1, Application US/08956657 ; Patent No. 6210917 ; GENERAL INFORMATION: APPLICANT: No. 6210917ori et al., Tsutomu TITLE OF INVENTION: METHOD FOR DETECTION ( TITLE OF INVENTION: METHYLTHICADENOSINE PI ; UMBER OF SEQUENCES: 1 ; CORRESPONDENCE ADDRESS: ; ADDRESSEE: Fish & Richardson P.C. ; STREET: 4225 Executive Square, Suite 14( ; CITY: La Jolla ; COUNTRY. II S.A. SD CURRENT APPLICATION: APPLICATION: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Vacuum CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/956,657 FILING DATE: CLASSIFICATION: PRIOR APPLICATION: APPLICATION: Query Match Best Local Simi Matches 141; TELEFAX: 619/67 INFORMATION FOR SEQ SEQUENCE CHARACTER LENGTH: 3083 ba TYPE: nucleic a STRANDEDNESS: 8 APPLICATION NUMBER: 08/827,342 FILING DATE: PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/176,855 FILING DATE: 29-DEC-1993 ATTORNEY/AGENT INFORMATION: NAME: Taylor, Stacy L. REGISTRATION NUMBER: 34,842 REFERENCE/DOCKET NUMBER: 07340/05000 TELECOMMUNICATION INFORMATION: TELEPHONE: 619/678-5070 TELEPHONE: 619/678-5099 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3083 base pairs TYPE: nucleic acid CTERNORDESC. Gingle -80 COUNTRY: U.S ZIP: 92037 COMPUTER READAB MEDIUM TYPE: COMPUTER: IB TOPOLOGY: CA CA 100.0%; ilarity 100.0%; Conservative ( U.S.A. linear 6210917ori et al., Tsutomu ON: METHOD FOR DETECTION OF ON: METHYLTHIOADENOSINE PHOSPHORYLASE DEFICIENCY IN MAMMOLIAN ON: CELLS single 07340/050001 Score 141; DB 3; Pred. No. 6.8e-33; Mismatches 0; Version #1.30 1400 Length 3083;

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APPLICANT: Carrera, Carlos J.
APPLICANT: The Regents of the University of
TITLE OF INVENTION: Method for Early Diagnorm of the University of
TITLE OF INVENTION: Prognosis in, Cancer
FILE REFERENCE: 023070-108010US
CURRENT APPLICATION NUMBER: US/09/335,231
CURRENT FILING DATE: 1999-06-17
PRIOR APPLICATION NUMBER: US 60/090,411
PRIOR FILING DATE: 1998-06-23
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TITLE OF INVENTION: METHOD FOR SELECTIVE METHIONINE
TITLE OF INVENTION: STARVATION OF MALIGNANT CELLS IN M.
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: PD28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5110
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/176,413
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                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                           IMMEDIATE
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OPERATING
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LOCATION:
                                                                                                                                  Local Similarity
les 140; Conser
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                                                                                                                                                                                                                                                                            LENGTH: 2763 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                CLONE:
                                                                                                                                                                                                                                                                TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: UZIP: 90067
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                                                                                 TCAAAATCTGGTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATAT
AAGTAGCATGGCTGCCCAG 141
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                                                                                                                                            98.9%;
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                                                                                                                                            Score 139.4; DB Pred. No. 2e-32;
                                                                                                                                Mismatches
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                                                                                                                                                         DB 1;
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                                                                                                                                                         Length 2763;
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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                NAME: HOWELLS, STACY L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 0734
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
TELEFAX: (619) 678-5099
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2763 base pairs
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Sequence 1, Patent No.
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LOTTAM, Howard B.

LPPLICANT: No. 58405050ri, T81

TITLE OF INVENTION: METHOD FORTITLE OF INVENTION: ACTORNATION SEQUENCY

CORRESPONDENT

ADDROGRAM
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MOLECULE TYPE: DN
MOLECULE SOURCE:
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CLASSIFICATION:
ATTORNEY/AGENT IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,54
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P
STREET: 4225 Executive Square,
                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                        NAME/KEY:
LOCATION:
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CITY: La
STATE: C
COUNTRY:
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Local Similarity 99.3%;
les 140; Conservative
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STRANDEDNESS: single
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APPLICANT: APPLICANT: APPLICANT:

No. 6214571ori, T Carson, Dennis A. Carrera, Carlos J

Tsutomu

INFORMATION:

Application US/09199137 214571

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RESULT 6
US-09-199-137-1
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REFERENCE/DOCKET NUMBER: 9D305
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2763 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: methv1--
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Best Local S
Matches 140
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Volume of the compation of the comp
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CLASSIFICATION PRIOR APPLICATION
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ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
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LOCATION:
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T: Carson, Dennis A.
T: Takabayashi, Kenji
INVENTION: METHOD FOR DETECTION OF
INVENTION: METHYLTHIOADENOSINE PHOSPHATASE DEFICIENCY IN MAMMALIAN
INVENTION: CELLS
F SEQUENCES: 5
NDENCE ADDRESS:
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California
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                                                                                                                                                                                                                                                                                                                                                                                                                 TCAAAATCTGGTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATAT
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1880 Century Park East, Suite 500
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larity 99.3%;
Conservative
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Pred. No. 2e-32;
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; NAME/KEY:
; LOCATION:
US-09-199-137-1
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US-08-227-800A-14
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Best Local S
Matches 140
                                                                 Patent No.
GENERAL II
                                                                                        Sequence
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TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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TITLE OF IN
TITLE OF IN
APPLICANT:
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NUMBER OF S
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IMMEDIATE SOUR
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CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: US 0
FILING DATE: 29-DEC-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 90067
COMPUTER READABLE
MEDIUM TYPE: F1
                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Howells, Stacy L. REGISTRATION NUMBER: 34 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nuclei
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                             CLONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 2
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
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                                            CANT: CARSON,
CANT: NOBORI,
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                                                                              14, Application
6689561
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                                                                                                                                                                                                                                                                                             Similarity
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          INVENTION:
INVENTION:
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Suite 500
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RESULT 8
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NAME: HOWELLS, STACY L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 0734
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 2763 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
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Best Local S
Matches 140
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-08-227-800A-1
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ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
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Local Similarity 99.3%;
les 140; Conservative
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
JRRENT APPLICATION DATA:
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        NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
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COMPUTER
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b. 6689864
INFORMATION:
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                                                                                                                          F: Carson, Dennis A.

No. 6689864ori, Tsutomu

INVENTION: Tumor Suppressor Gene and Methods for

Detection of Cancer, Monitoring of Tur

Cancer Treatment
READABLE FORM:
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PCT-US94-14919-1
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           Sequence 1, Application PC/TUS9414919
GENERAL INFORMATION:
APPLICANT: THE REGENTS OF THE UNIVE
APPLICANT: OF CALIFORNIA
TITLE OF INVENTION: METHOD FOR SELE
TITLE OF INVENTION: STARVATION OF M.
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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Best Local S
Matches 140
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SEQUENCE DESCRIPTION: SEQ
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TELEFAX: (415) 576-0300
MATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 2763 base pairs
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APPLICATION NUMBER: US 0
FILING DATE: 20-AUG-1997
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US/08/921,954

FILING DATE: 26-Aug-1997

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/908,671A
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STRANDEDNESS: single
TOPOLOGY: linear
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OTHER INFORMATION: /
methylthioadenosine [
(MTAse) genomic nucle
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LOCATION:
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Robbins,
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REGISTRATION NUMBER: 20,121
REFERENCE/DOCKET NUMBER: 555-286
TELECOMMUNICATION INFORMATION:
TELEPHONE: 213-977-1001
TELEFAX: 213-977-1003
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2763 base pairs
TYPE: nucleic acid
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Best Local S
Matches 140
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, V

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14919
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                      APPLICANT:
APPLICANT:
TITLE OF IN
TITLE OF IN
                          ZIP: 90012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                     NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Robbins, Berliner & Carson
STREET: 201 N. Figueroa Street, 5th Floor
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                                                            STREET: 20-
STREET: 20-
CITY: Los Angeles
California
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                                                     COUNTRY:
ZIP: 900
   COMPUTER:
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LOCATION:
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California
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PE: Floppy disk
IBM PC compatib
SYSTEM: PC-DOS/
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Conservative
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PC-DOS/MS-DOS
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TGGCTGCCCAG 415

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APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: ESTS and En

FILE REFERENCE: GENSET.054PR2

CURRENT APPLICATION NUMBER: US/

CURRENT FILING DATE: 2000-07-2

NUMBER OF SEQ ID NOS: 19335

SOFTWARE: Patent.pm

SEQ ID NO 17307

LENGTH: 499
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US-09-621-976-17307
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LOCATION:
PCT-US94-14920-1
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REFERENCE/DOCKET NUMBER: 5555
TELECOMMUNICATION INFORMATION:
TELEPHONE: 213-977-1001
TELEFAX: 213-977-1003
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2763 base pairs
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ORGANISM: Homo
09-621-976-17307
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                                                                      42.7%;
Similarity 89.0%;
55; Conservative
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Jobert, S.
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                                      CCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAAAGTAG
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CATGGCTGCCCAG 141
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US-09-513-999C-31128
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Best Loc
Matches
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APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence
Patent No. 6783961
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,9
CURRENT FILING DATE: 2000-02-24
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Sequence 1, Application US/09198452A
Patent No. 6559294
GENERAL INFORMATION:
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SEQ ID NO 31128
LENGTH: 313
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APPLICANT: Dumas Milne
APPLICANT: Duclert, A
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                   ORGANISM: Chlamydia pneumoni FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(15000)
OTHER INFORMATION: n=a or c
NAME/KEY: misc_feature
LOCATION: (15001)..(30000)
OTHER INFORMATION: n=a or c
NAME/KEY: misc_feature
LOCATION: (30001)..(45000)
OTHER INFORMATION: n=a or c
NAME/KEY: misc_feature
LOCATION: (45001)..(60000)
OTHER INFORMATION: n=a or c
NAME/KEY: misc_feature
LOCATION: (60001)..(75000)
OTHER INFORMATION: n=a or c
NAME/KEY: misc_feature
LOCATION: (75001)..(90000)
OTHER INFORMATION: n=a or c
NAME/KEY: misc_feature
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APPLICANT: Griffais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic s
TITLE OF INVENTION: thereof and uses thereof, in
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT APPLICATION NUMBER: US/09/198,452A
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ORGANISM: Homo sapiens
09-513-999C-31128
            LOCATION:
OTHER INFO
NAME/KEY:
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Similarity 98.0%;
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misc_feat (90001).
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NAME/KEY: misc feature
LOCATION: (12001)..(13000)
OTHER INFORMATION: n=a or c or
NAME/KEY: misc feature
LOCATION: (135001)..(15000)
OTHER INFORMATION: n=a or c or
NAME/KEY: misc feature
LOCATION: (150001)..(18000)
OTHER INFORMATION: n=a or c or
NAME/KEY: misc feature
LOCATION: (165001)..(18000)
OTHER INFORMATION: n=a or c or
NAME/KEY: misc feature
LOCATION: (180001)..(21000)
OTHER INFORMATION: n=a or c or
NAME/KEY: misc feature
LOCATION: (195001)..(21000)
OTHER INFORMATION: n=a or c or
NAME/KEY: misc feature
LOCATION: (210001)..(225000)
OTHER INFORMATION: n=a or c or
NAME/KEY: misc feature
LOCATION: (225001)..(240000)
OTHER INFORMATION: n=a or c or
NAME/KEY: misc feature
LOCATION: (225001)..(255000)
OTHER INFORMATION: n=a or c or
NAME/KEY: misc feature
LOCATION: (230001)..(285000)
OTHER INFORMATION: n=a or c or
NAME/KEY: misc feature
LOCATION: (230001)..(315000)
OTHER INFORMATION: n=a or c or
NAME/KEY: misc feature
LOCATION: (330001)..(345000)
OTHER INFORMATION: n=a or c or
NAME/KEY: misc feature
LOCATION: (330001)..(345000)
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NAME/KEY: misc feature
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NAME/KEY: misc feature
LOCATION: (345000)...(345000)
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LOCATION: (375001)..(390000)
OTHER INFORMATION: n=a or c or
NAME/KEY: misc feature
LOCATION: (390001)..(405000)
OTHER INFORMATION: n=a or c or
NAME/KEY: misc feature
LOCATION: (405001)..(420000)
OTHER INFORMATION: n=a or c or
NAME/KEY: misc feature
LOCATION: (420001)..(435000)
OTHER INFORMATION: n=a or c or
NAME/KEY: misc feature
LOCATION: (435001)..(450000)
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NAME/KEY: misc feature
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Carson, Dennis A.

LEPLICANT: Carrera, Carlos J.

APPLICANT: The Regents of the University (
TITLE OF INVENTION: Method for Early Diagn
TITLE OF INVENTION Prognosis in, Cancer
FILE REFERENCE: 023070-108010US
CURRENT APPLICATION NUMBER: US/09/335,231
CURRENT FILING DATE: 1999-06-17
PRIOR APPLICATION NUMBER: US 60/090,411
PRIOR FILING DATE: 1998-06-23
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver.
SEQ ID NO 24
LENGTH: 32
TYPE: DNP
ORGANT
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US-09-3
RESULT 15
US-08-998-416-302
; Sequence 302, Application
; Patent No. 6239264
; GENERAL INFORMATION:
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Similarity 56.6%;
50; Conservative
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REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 302:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Value of the compation 
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ORIGINAL SOURCE:
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completed: 1
le : 45.1846
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Research Triangle Park
: No. 6239264th Carolina
RY: USA
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I: Pohlmann, Au-
I: Pohlmann, Au-
I: Steiner, Sabine
I: Steiner, Sabine
I: Mohr, Christine
I: Wendland, Jurgen
II: Wendland, Jurgen
II: Knechtle, Philipp
II: Rebischung, Corinne
II: Rebischung, Corinne
INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
INVENTION: AND USES THEREOF
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DNESS: single
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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

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9: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*

12: /cgn2_6/ptodata/1/pubpna/US09D_PUBCOMB.seq:*

13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*

14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

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US-10-779-476-2

US-10-367-366-1

US-10-017-721-3

US-10-235-192A-48

US-10-282-122A-11017

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Sequence 1, Appli
Sequence 25, Appl
Sequence 14, Appl
Sequence 3235, Ap
Sequence 749, Appli
Sequence 2, Appli
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Sequence 48, Appl
Sequence 11017, A
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## ALIGNMENTS

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RESULT 1

Sequence 1, Application US/09780114

Sequence 1, Application US/09780114

Patent No. US20020146695Alori, Tsutomu
Carson, Dennis A.
Takabayashi, Kenji
TITLE OF INVENTION: Method for Detection of the Presence or Absence of Methylthioadenosine Phosphorylase
(MTASe) in a

NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ADDRESSEE: Townsend and Townsend and Crew LLP
STATE: P4111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATION SYSTEM: C-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/09/780,114
FILING DATE: 09-Feb-2001
CLASSIFICATION NUMBER: US/09/780,114
FILING DATE: 04-May-1998
APPLICATION NUMBER: US/09/772,914
FILING DATE: US-DEC-1993
APPLICATION NUMBER: US 08/176,855
FILING DATE: US -DEC-1993
APPLICATION NUMBER: US 08/459,343
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NUMBER: (

02-JUN-1995 NUMBER: US 08/8 26-MAR-1997

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hes 141;
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ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 0230
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
ORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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LOCATION: 2838..2876
OTHER INFORMATION: /note= '
SEQUENCE DESCRIPTION: SEQ ID NO:
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LOCATION: 1764..1953
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LOCATION: 1..3083
OTHER INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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RESULT 2
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; Publication No. US200;
; GENERAL INFORMATION:
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APPLICANT: Schmid, Mathias
APPLICANT: Schmid, Mathias
APPLICANT: Schmid, Mathias
APPLICANT: Carrera, Carlos J.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Method for Early Diagnosis of, and Determination of
TITLE OF INVENTION: Prognosis in, Cancer
FILE REFERENCE: 023070-108010US
CURRENT APPLICATION NUMBER: US/10/326,681
CURRENT FILING DATE: 2003-04-15
PRIOR APPLICATION NUMBER: US 60/090,411
PRIOR FILING DATE: 1998-06-23
PRIOR FILING DATE: 1998-06-23
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SOFTWARE: PatentIn Ver.
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LOCATION: (450)..(
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LOCATION: (1)..(3083)
OTHER INFORMATION: n = unknown
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NAME/KEY: exon
LOCATION: (2426)..(2548)
OTHER INFORMATION: exon
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ORGANISM: Homo sapiens
                                                                                                                                                                              LOCATION: (2838)..(2876)
OTHER INFORMATION: exon
                                                                                                                                                                                             NAME/KEY: exon
LOCATION: (283)
                                                                                                                                                                                                                                                                                                                                 NAME/KEY: exon
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LOCATION: (899)..(1066)
OTHER INFORMATION: exon
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LOCATION: (119)..(151)
OTHER INFORMATION: exon 1
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                                                                                                                                                                                                                                                                                                                 LOCATION: (1764)..(1953)
OTHER INFORMATION: exon
                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: exon
LOCATION: (1378)..(1480)
OTHER INFORMATION: exon
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NAME/KEY: exon
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LENGTH: 3083
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                                 2754
                                                                                          100.0%;
Similarity 100.0%;
11; Conservative 0;
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CTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACAT
                                TCAAAATCTGGTTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATAT
                                                    TCAAAATCTGGTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATAT
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                                                                                                                                                                                 exon 8
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                                                                                               Score 141; DB 15; Pred. No. 3e-31; Mismatches 0;
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RESULT 3
US-09-908-671-14
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                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/227,800
FILING DATE: 14-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: HOWELLS, STACY L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07340/023001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 14, Application US/09908671 Publication No. US20030138928A1 GENERAL INFORMATION:
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                                                                                                                                                                  Best
                                                                                                                                                      Matches
                                                                                                                                                   Local Sinhes 140;
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Ve.

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/908,671

FILING DATE: 18-Jul-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                      LENGTH: 2763 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: Methylthioadenosir
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                                                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: 1..2763
SEQUENCE DESCRIPTION: SEQ
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                               2248
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  121
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Similarity 99.3%;
O; Conservative
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STREET: 42
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                           CACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACAT
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STATE: California
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 TAAAGTAGCATGGCTGCCCAG
                                                                                         AATCAAAATCTGTTTTTTTTTTAACAAACATCTCAGTAATTA
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ATION:
CARSON, DENNIS A.
NOBORI, TSUTOMU
NOBORI, TSUTOMU
TUMOR SUPPRESSOR GENE AI
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Pred. No. 8.5e-31;
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APPLICANT: Thiagalingam, Arunthathi
APPLICANT: Lewis, Marcia E.
TITLE OF INVENTION: Nucleic Acid Sequences Differentially
TITLE OF INVENTION: Expressed in Cancer Tissue
FILE REFERENCE: 1657/1032
CURRENT APPLICATION NUMBER: US/09/969,034
CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/237,271
PRIOR APPLICATION NUMBER: 60/237,271
PRIOR FILING DATE: 2000-02-10
NUMBER OF SEQ ID NOS: 4494
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3235
LENGTH: 603
TYPE: DNA
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                                                                       APPLICANT: Ruben et al.

TITLE OF INVENTION: Colon and Colon Cancer As

FILE REFERENCE: PA005P1

CURRENT APPLICATION NUMBER: US/10/106,698

CURRENT FILING DATE: 2002-03-27

PRIOR APPLICATION NUMBER: PCT/US00/26524

PRIOR FILING DATE: 2000-09-28

PRIOR APPLICATION NUMBER: US 60/157,137

PRIOR APPLICATION NUMBER: US 60/157,137

PRIOR APPLICATION NUMBER: US 60/163,280

PRIOR FILING DATE: 1999-09-29

PRIOR FILING DATE: 1999-11-03

NUMBER OF SEQ ID NOS: 8564

SOFTWARE: Patentin Ver. 3.0
US-10-106-
                                                                                                                                                                                                                                                                                                         Sequence 749, Publication No
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Best Local
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                                                           SOFTWARE: Pat
SEQ ID NO 749
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LOCATION: 492, 497, 506, 527, 542,
OTHER INFORMATION: n = A,T,C or G
09-969-034-3235
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ORGANISM: Homo
0-106-698-749
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                               TYPE:
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Local Similarity 96.9%;
nes 63; Conservative
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Astle, Jon H.
Carroll, Eddie III
Catino, Theodore J.
Dwivedi, Poornima
Molino, Gary A.
Thiagalingam, Arunth
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Application US/09969034
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Pred. No. 3.7e-08;
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LENGTH: 2269
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           SOFTWARE:
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APPLICANT: Leoni, Lorenzo M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION AND TREATMENT
TITLE OF INVENTION: METHYLTHIOADENOSINE PHOSPHORYLASE DEFICIENT CANCERS
FILE REFERENCE: 076936-0307942
CURRENT APPLICATION NUMBER: US/10/779,476
CURRENT FILING DATE: 2004-02-13
PRIOR APPLICATION NUMBER: 60/447,888
PRIOR FILING DATE: 2003-02-14
PRIOR APPLICATION NUMBER: 60/460,715
PRIOR APPLICATION NUMBER: 60/460,715
PRIOR FILING DATE: 2004-04-04
NUMBER OF SEQ ID NOS: 12
                                APPLICANT: Skalitzky, Donald TITLE OF INVENTION: Combination Therapies For ITLE OF INVENTION: Phosphorylase Deficient FILE REFERENCE: PC19080A (AG110-01) CURRENT APPLICATION NUMBER: US/10/367,366 CURRENT FILING DATE: 2003-02-14 NUMBER OF SEQ ID NOS: 3
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.0-779-476-2
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LENGTH:
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Similarity 89.0%;
55; Conservative
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Bloom,
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Boritzki, Theod
Ogden, Richard
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Kung, Pei-Pei
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Laura A
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Pred. No. 1.8
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; ORGANISM: Homo sapiens
US-10-017-721-3
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Matches 67
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             SEQ ID NO LENGTH:
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                                                                                                           APPLICANT: McCarthy, Jeanette
TITLE OF INVENTION: Methods and Compositions for Identifying
TITLE OF INVENTION: Risk Factors for Abnormal Lipid Levels
TITLE OF INVENTION: and Disorders Associated Therewith
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CURRENT APPLICATION NUMBER: US/10/017,7:
CURRENT FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: US 60/317,033
PRIOR FILING DATE: 2001-09-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: McCarthy, Jeanette
APPLICANT: Daley, George
APPLICANT: Bolk, Stacey
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT
                                                       NUMBER OF SEQ
                                                                 FILE REFERENCE: MMI-011
CURRENT APPLICATION NUMBER:
CURRENT FILING DATE: 2002-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/330,248
PRIOR FILING DATE: 2001-10-17
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4
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                                     SOFTWARE:
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ORGANISM:
FEATURE:
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59; Conservative
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Similarity 58.3%;
57; Conservative
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Pred. No. 7.3e-06;
D; Mismatches 8;
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US-10-282-122A-
; Sequence 1101
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Sequence 11017, Application US/10282122A
Publication No. US20040029129A1
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NUMBER OF
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                                                                                           GANISM: Borrelia
282-122A-11017
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R FILING DATE: 2000-12-22
R APPLICATION NUMBER: 60/2
R FILING DATE: 2000-12-22
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                                                                                                                                                                                                FILING DATE: 2001-0 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/206,848 FILING DATE: 2000-05-23 APPLICATION NUMBER: 60/207,727
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  229
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Trawick, John
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Zyskind, Jud
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                       TTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATATCACTGCCTCCTTTCTT
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR APPLICATION NUMBER: US 60/185,363

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-027-632-293; Sequence 29329, Publication No.; GENERAL INFORMA
                                                    APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

FILE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/156,358
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IG DATE: 1999-08-09

EQ ID NOS: 325720

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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Maj
TITLE OF INVENTION: Polymorphisms in the
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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OR APPLICATION NUMBER: US 60/218,006
OR FILING DATE: 2000-07-12
OR APPLICATION NUMBER: US 60/198,676
OR FILING DATE: 2000-04-20
OR APPLICATION NUMBER: US 60/193,483
OR FILING DATE: 2000-03-29
OR APPLICATION NUMBER: US 60/185,218
OR APPLICATION NUMBER: US 60/185,218
OR FILING DATE: 2000-02-24
OR APPLICATION NUMBER: US 60/167,363
OR FILING DATE: 1999-11-23
OR APPLICATION NUMBER: US 60/156,358
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FILING DATE: 1999-08-09
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DR APPLICATION NUMBER: US 60/193,483
DR FILING DATE: 2000-03-29
DR APPLICATION NUMBER: US 60/185,218
DR FILING DATE: 2000-02-24
DR APPLICATION NUMBER: US 60/167,363
DR FILING DATE: 1999-11-23
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DR APPLICATION NUMBER: US 60/167,363

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## ALIGNMENTS

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le,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gayle,P., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J.ckenbush,J.
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGN"
/note="Vector: pBluescriptSKm"
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Seq primer: puc 18 forward
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BX390237 900 bp
BX390237 Homo sapiens PLACENTA CC
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
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/dev_stage="Adult"
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                          Fobo, G., Han, M. and Wiemann, S.
EST (Koehrer, K., Beyer, A., Mewes, H.W., Weil, B., Ar
Unpublished (2003)
Contact: MIPS
MIPS
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DKFZp779E0622_r1 779 (synonym: r
DKFZp779E0622_5', mRNA sequence.
BX495614
BX495614.1 GI:32010447
EST.
Homo sapiens (human)
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five puend enriched, double-strand cDNA was digested with Not I and clainto the Not I and EcoR V sites of the pCMVSPORT 6 vector. Libra was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence clusters for more information - Library was constructed by Life Technologies, a sequence information - Library was constructed belongs to sequence clusters.
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On May 8, 2003 this sequence version replaced Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CS0BAG024ZA09_CS02273_1&c=5445.f
Ingolstaedter Landstr.1, D-85764 Neuherberg, This is the 5' sequence of the clone insert
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and Ecor V
sites of the pCMVSPORT 6 vector. Library was normalized.'
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/db_xref="taxon:9606"
/clone="CS0DI002YH04"
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Eutheria;
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by BMFZ (Biomedical Research Center at the Heinrich-Heine-University, Duesseldorf/Germany) within the cDNA sequencing consortium of the German Genome Project. No sl sequence available. This clone (DKFZp779E0622) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                        cDNA Library Preparation: Life Technologies, InccDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1521 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 246.
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AI919501
AI919501.1 GI:5639356
                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
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/dev_stage="fetal"
/lab_host="DH10B"
/clone_lib="779 (syno)
'clone="IMAGE:2188489"
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Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jos Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. WashU-NCI human EST Project
Unpublished (1997)
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)e10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1031274
)imilar to TR:G847724 G847724 METHYLTHIOADENOSINE PHOSPHORYLASE
                                                                                                                                                                                                                                                                                                                                                                                                          l: est@watson.wustl.edu clone is available royalty-free through LLNL; Consortium (info@image.llnl.gov) for further; ble reversed clone: similarity on wrong strand primer: -40ml3 fwd. ET from Amersham
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Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wilson RK
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/note="Organ: stomach; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.69 kb. Life Technologies catalog #:
11549-011"
                                                                                                                                 /clone_lib="Soares_testis_NHT"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(c
                                                                                                organism="Homo
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                                                                                                                                                                                                                                                                                              mol_type="mRNA"
db_xref="taxon:9606"
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nes 65; Conservative
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anat Tumor Gene Index
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UI-H-FT2-bjn-i-17-0-UI.s1 NCI_CGAP_UI-H-FT2-bjn-i-17-0-UI 3', mRNA sec_CD364939
CD364939.1 GI:31149029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of
cDNA Library Arrayed by: Dr. M. Bento Soares, University of I
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cgap.html
Seq primer: M13 FORWARD
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/dev stage="Adult"
//lab_host="DH10B (Life Technologies)"
//clone lib="NCI CGAP FT2"
//note="Organ: Lung; Wector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP FT2 is a subtracted cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; EPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Klebsiella moi 500, 24 hours; Meanoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; Wt adenovirus moi 500, 3 hours; Wt adenovirus + LPS 24 hours; The library was subtracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue
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/db_xref="taxon:9606"
/clone="UI-H-FT2-bjn-i-17-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologie
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Transcriptome characterization elucidates signaling networks control human ES cell growth and differentiation

Nat. Biotechnol. 22 (6), 707-716 (2004)

Contact: Brandenberger R

Regenerative Medicine

Geron Corporation

230 Constitution Drive, Menlo Park, CA 94025, USA

Tel: 650 473 8658
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                           Conservative
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Length: 612 Std Error:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                               Length:
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of Iowa.
TAG_TISSUE=Human Lung A
TAG_LIB=UI-H-FT2
TAG_SEQ=GGCCATGCCG"
                                                                                                                                                                            /clone_lib="GRN_PREHEP"
/note="oligo dT_primed, full-length enriched cDNA
from DMSO-treated hES cell line H9 (p22) maintaine
feeder-free conditions"
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mol_type="mRNA"
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89.0%;
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286
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Pred. No. 3.2e-06;
); Mismatches 8;
                                                                                                                      Score 60.2; DB 7
Pred. No. 3.2e-06
                                                                                                           Mismatches
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RESULT 10
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Korea Research Institute of
52 Eoeun-dong Yuseong-gu, 1
Tel: +82-42-860-4470
Fax: +82-42-860-4409
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Kim, N.S., )
    CD364946
UI-H-FT2-bjn-k-07-0-UI.81
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Plate: 32 row: F column: 01
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
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BM784030
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K-EST0062086
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                     CCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAAAGTAG
                                                                                                                                                                                   CCTCCATAACCTGAAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAAAGTA
                                                                                                                                               CATGGCTGCCCAG 141
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sapiens
                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                  /Cell_line="SCattering floating"
/cell_line="SNU-620"
/lab_host="Top10F'"
/clone_lib="S6SNU620"
/clone_lib="S6SNU620"
/clone_lib="S6SNU620"
/clone_lib="S6SNU620"
/clone_lib="S6SNU620"
/note="Organ: Stomach; Vector: pCNS; Site_l: EcoRI;
Site_2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."
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s 1 to 681)
, Hahn,Y., Oh,
Cheong,J.E.,
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db_xref="taxon:9606"
clone="S6SNU620-32-F01"
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Pred. No. 3.3e-06;
D; Mismatches 8;
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Sohn,H.Y., Kim,
684 bp
1 NCI_CGAP_
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Daejeon 305-333, South Korea
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J.M., Park, H.S., Kim,
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    CDNA clone
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Unpublished (1907
Contact
                                                                                                                                                                       65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cgap.html
Seq primer: M13 FORWARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo
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-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.conal Cancer Institute, Cancer Genome Anal
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                                        TGGCTGCCCAG 141
                                                                                sapiens (human)
                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                        /dev stage="Adult"

/lab_host="DH10B (Life Technologies)"

/clone lib="NCI_CGAP_FT2"

/note="Organ: Lung; Vector: pT773-Pac (Pharmacia) with a modified polylinker; Site_1: ECOR I; Site_2: Not I; NCI_CGAP_FT2 is a subtracted cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; pMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 3 hours; Staph aureus moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 500, 3 hours; Madenovirus moi 500, 3 hours; Wt adenovirus moi 500, 24 hours; wt adenovirus moi 500, 24 hours; wt adenovirus hours; wt adenovirus hours; wt adenovirus hours; the library was subtracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University
                                                                                                                                                                                                                                                                                                                                                     was
                                                                                                                                                                                                                                                                                  TAG_TISSUE=Human Lu:
TAG_LIB=UI-H-FT2
TAG_SEQ=GGCCATGCCG"
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/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
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/db_xref="taxon:9606"
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89.0%;
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Pred. No. 3.3e-06;
); Mismatches 8;
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Eukaryota; Metazoa; Choro
Mammalia; Eutheria; Prima
1 (bases 1 to 836)
Ansorge, W., Wirkner, U., 1
EST (Ansorge, et al.)
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602310222F1 NIH_MGC_8
mRNA sequence.
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DKFZp586O1023 rl 5

DKFZp586O1023, mRN

AL048242

AL048242.1 GI:472
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Mammalia; E
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NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health,
Unpublished (1999)
                                                                                    Homo
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10108 row: k column: 06
High quality sequence stop: 667.
Location/Qualifiers
                                                                                                     EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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65; Conserv
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sapiens
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sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                /clone="IMAGE:4401533"
/tissue_type="duodenal adenocarcinoma, cell line"
/lab_host="DH10B {phage-resistant}"
/clone_lib="NIH_MGC_88"
/note="Organ: small_intestine; Vector: pCMV-SPORT6;
Site_1: NotI; Site_2: SalI; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH_MGC Library."
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1 to 819)
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                                                                                                                 GI:4729075
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_xref="taxon:9606"
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                                             Chordata;
Primates;
                                                                                                                                           sequence
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Pred. No. 3.4e-06;
0; Mismatches 8
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                    Mewes, H.W
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Catarrhini;
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Catarrhini;
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                    Gassenhuber
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i; Hominidae;
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                    Wiemann,
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E 1 (bases 1 to 836)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTP

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

niramins72 row: k column: 18
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Homo gar
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No s1 sequence available.

This clone (DKFZp58601023) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

Location/Qualifiers
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This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
sequenced by EMBL (European Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BG574734 836 bp mRNA linear EST 10-APR-2001 602596770F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:4705673 5', mRNA sequence.
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Contact: MIPS
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                                                                                          Plate: LLAM10572 row: k co
High quality sequence stop:
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larity 89.0%;
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="586 (synonym: hutel)"
/note="Vector: pSport1; Site_1: NotI; Site_2:
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4705673"
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0; Mismatches 8;
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Mammalia; Eutheria; Primates; C
1 (bases 1 to 903)
Li,W.B., Gruber,C., Jessee,J. a
Full-length cDNA libraries and
Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five plend enriched, double-strand cDNA was digested with Not I and clointo the Not I and EcoR V sites of the pCMVSPORT 6 vector. Librawas normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluste
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BX371508 Homo sapiens PLACENTA COT
Clone CS0DI002YH04 3-PRIME, mRNA se
BX371508
BX371508.1 GI:30448046
EST.
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                                                                             similarity 89.0%;
65; Conservative
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Similarity 89.0%;
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                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODIO02YH04"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_87"
/note="Organ: breast; Vector: pCMV-SPORT6; Site_1: NotI
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.383 kb. Library enriched for
full-length clones and constructed by Life Technologies
Note: this is a NIH_MGC Library."
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25-NORMALIZED Homo sapiens cDNA
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1 (bases 1 to 911)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On May 5, 2003 this sequence version replaced gi:30377483.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                There is a virtual cDNA representing this cluster. For more information about this cluster and the virtual cDNA, see http://www.genoscope.cns.fr/cdna?s=CSOBAIO16ZBO8_CSO1498_2&c=340.r.Location/Qualifiers
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il: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
strand cDNA was digested with Not I and cloned
enriched, double-strand cDNA was digested with Not I and cloned
the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
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ision of Invitrogen. This sequence belongs to sequence cluster
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/clone="CSODI002YH06"

/tissue_type="PLACENTA COT 25-NORMALIZED"

/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT)

/note="1st strand cDNA was primed, double-strand cDNA was primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
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Eukaryota; Metazoa; Chordata,
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(CE 1 (bases 1 to 383)

NRS Nobori, T., Takabayashi, K., Tran, P., Orvis, L., Bara
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Genomic cloning of methylthioadenosine phosphorylase: a puri
metabolic enzyme deficient in multiple different cancers

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L42633.1:1. .303,1. .383)
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/gene="MTAP"
/product="methylthioadenosine phosphorylase"
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Edwards, J.-B.D.M., Jobert, S. and Giorda
EST's and encoded human proteins
Patent: US 6639063-A 17307 28-OCT-2003;
Location/Qualifiers
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                     Dumas Milne Edwards, J.B., ESTs and encoded human pr Patent: EP 1104808-A 1730
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39; Conservative 0
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            (FR)
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/product="methylthioadenosine phosphorylase"
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/db_xref="GI:38570318"
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LRCHSKGTMVTIEGPRFSSRAESFMFRTWGADVINMTTVPEVVLAKEAGICYASIAMG
TDYDCWKEHEEAVSVDRVLKTLKENANKAKSLLLTTTIPQIGSTEWSETLHNLKNMAQF
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/organism="unknown|
/mol_type="genomic
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Catarrhini;
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                                               Giordano, J.Y
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acmo sapiens full open reading figene MTAP, methylthicadenosine phetopcodon.
CR541670
CR541670.1 GI:494567
Full ORF shutt
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Edwards, J.B.D.M., Jobert, S. and Giordano, J.E.

EST and encoded human protein

Patent: JP 2002010789-A 13440 15-JAN-2002;

GENSET CORP

OS Homo sapiens (human)

PN JP 2002010789-A/13440

PD 15-JAN-2002

PF 07-AUG-2000 JP 2000280989

PF 07-AUG-1999 US 60/147499

PI JEAN BAPUTIST DUMAS MILNE EDWARDS, SEVELIN

GIORDANO

PC C12N15/09, C12N15/09, C07K14/47, C07K16/18, C1

C12N1/21,

PC C12N5/10, C12P21/02, C12P21/08, C12Q1/68, C12N

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CC EST and encoded human protein

FH Key

FT source

// Organism='Homo sapiens (h
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JP 2002010789-A/13440.
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JP 2002010789-A/13440
15-JAN-2002
07-AUG-2000 JP 2000280989
05-AUG-1999 US 60/147499
JEAN BAPUTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE
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larity 100.0%; Pred. No. 0.00065;
Conservative 0; Mismatches 0;
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Location/Qualifiers
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The CDS has been inserted into pDONR201 via a BP Clonase(TM) reaction. Additional sequence has been added in front of the st codon: att. .AAAAAA GCA GGC TCC ACC (ATG).
The stopcodon is followed by the 3' att site: GACCCAGCTTTCTT..
The clone is validated by full sequence check.
Compared to the reference sequence NM_002451 (GI:6006025) we fo AA exchange(s) at position (first base of changed triplet):
139(leu->met) 166(ile->val)
Clone distribution: http://www.rzpd.de/products/orfclones/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neubert, P., Kstrang, K., Schatten, R., S. Neubert, P., Kstrang, K., Schatten, R., S. Korn, B., Zuo, D., Hu, Y. and LaBaer, J. Direct Submission
Submitted (28-JUN-2004) RZPD Deutsches Genomforschung GmbH, Im Neuenheimer Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia;
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                                 In 100.0%;
Similarity 100.0%;
39; Conservative 0
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Contact RZPD (customer.service@rzpd.de) for further information.
This CDS clone is part of a collection of human full ORF clones
jointly established and verified by the Harvard Institute of
Proteomics (HIP) and RZPD.
This CDS has been cloned incl. stopcodon.
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Unpublished
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Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
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                                                                                                                                                         /codon_start=1
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1 to 852)
                                                                                                                                                                                                                                                                                                                                                                                                                                clone="RZPDo834G1127D"
clone_lib="Human Full ORF
lab_host="DH5Alpha"
note="Vector: pDONR201, Si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Homo sapiens
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/db_xref="taxon:9606"
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Shen, B., He
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Henze,S., Mar,
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Mammalia; E
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Zehnder, L.R., Kuhn, L.A. and Meng, J.J.
Combination therapies for treating methylthicadenosine
phosphorylase deficient cells
Patent: WO 03074083-A 1 12-SEP-2003;
PFIZER INC. (US)
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AX826996.1
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Homo
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Direct Submission
Submitted (09-SEP-1996) The Sam and Rose Steir
                                                                                                                                                                                                               and Carson, D.A.
and Carson, D.A.
Genomic cloning of methylthioadenosine phosphorylase: a
metabolic enzyme deficient in multiple different cancers
metabolic enzyme deficient in S.A. 93 (12), 6203-6208 (1996)
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Similarity 100.0%;
39; Conservative 0;
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Location/Qualifiers
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Cloned MTAP cDNA"
                                                                                                  (09-SEP-1996) The Sam and Rose Stein Institute for aging, and Department of Medicine, University of at San Diego, La Jolla, CA 92093-0663, USA
                                     organism="Homo
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Pred. No. 0.00059;
Mismatches 0;
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S Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA segmences
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 USA
NIH-MGC
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Mammalia; E
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                                   Submitted (26-MAR-2002)
Gene Collection (MGC), (
Institute, 31 Center Dr.
                                                                                         Direct Submission
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Strausberg, R.
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'tissue_lib="lambda gt1
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note="putative"
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Primates;
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http://mgc.nci.nih.gov
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Pred. No. 0.0
; Mismatches
                                                    Cancer
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Catarrhini;
                              Institutes of Heamomics Office, Nata 11A03, Bethesda,
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0.00057;
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i; Hominidae;
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Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shira

Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Institute for Systems Biology

http://www.systemsbiology.org

contact: amadan@systemsbiology.org

Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha

Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                                                                                                                                               909
                                                                                Homo sapier
Eukaryota;
Mammalia; E
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This clone was selected for full length sequencing because passed the following selection criteria: matched mRNA gi: 6
Location/Qualifiers
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Email: cg
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Human methylthioadenosine
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                                                   Olopade, O.
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yling, M.H.,
lander, S.K.
struction of
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larity 100.0%;
Conservative 0,
                                                                                                                       sapiens
                                                                                                                                     sapiens (human)
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                                                1 to 2269)
.I., Pomykal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
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/protein_id="AAH26106.1"
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/db_xref="LocusID:4507"
/db_xref="MIM:156540"
                                                                                                                                                                        GI:847723
                                                                                  Metazoa; Chordata; Craniata; V
Eutheria; Primates; Catarrhini;
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/db_xref="LocusID:4507"
/db_xref="MIM:156540"
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/lab_hc
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|db_xref="taxon:9606"
|clone="MGC:33067 IMAGE:4820938"
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Gursky,S., Stadler,W.M.,
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ne_lib="NIH_MGC_95"
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 2.8-megabase yeast
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                                  Sveen, L.W., E, Le Beau, M.M.
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7604019
2 (bases 1 to 2269)
Olopade,O.I.
Direct Submission
Submitted (06-MAR-1995) Olufunmilayo I.
University of Chicago Pritzker School of Avenue, Chicago, IL 60637-1470, USA
Location/Qualifiers
1. .2269
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Sequence 1
AR059583
AR059583.1
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Carrera, C.J., Carson, D.A., Cottam, H.B. and Nobori, Method for inhibiting adenylosuccinate synthetase methylthicadenosine phosphorylase deficient cells Patent: US 5840505-A 1 24-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                          39;
      Similarity
39; Conservat
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larity 100.0%;
Conservative 0
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/db_xref="GI:847724"
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                                                                                                                  Location/Qualifiers
                                                                            organism="unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="MTAP"
|22. .973
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Score 39; pred. No. 0.0
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Sequence 14
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Sequence
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Carson,D.A. and Nobori,T.
Tumor suppressor gene and methods for detection of comonitoring of tumor progression and cancer treatment Patent: US 6689561-A 14 10-FEB-2004;
Location/Qualifiers
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Patent:
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Nobori,T. and Carson,D.A.
Method for selective methionine starvation
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larity 100.0%;
Conservative 0;
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1. .2763
/organism="unknown"
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Mismatches 0;
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Unclassified.

(bases 1 to 2763)

Carson, D.A. and Nobori, T.

Cyclin dependent kinase 4 inhibitor

Patent: US 6689864-A 14 10-FEB-2004;

Location/Qualifiers

1. 2763

/organism="unknown"
/mol_type="genomic DNA"

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Sequence
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                                                                      cancer
Patent:
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Unclassified.
1 (bases 1 to 3083)
Carson,D.A., Schmid,M. and Carrera,C.J.
Method for early diagnosis of, and determination
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39; Conservative 0
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ABQ56306 to ABQ60787 represent isolated nucleic acids (I) differentially expressed in cancer tissues. ABB78993 to ABB79004 represent proteins encoded by the ABQ60776 to ABQ60787 nucleic acid sequences. (I) can be used in antisense therapy. An antibody immunoreactive with a polypeptide encoded by (I) is useful for detecting cancer in a patient sample, and for detecting the presence or absence of a polynucleotide encoded by a nucleic acid which hybridises to (I) in a cell. A probe/primer derived from (I) can be used for determining the presence of a nucleic acid which

New isolated nucleic acid that is differentially expressed in cancer tissues useful for determining the presence of colon cancer in a cell tissue type, and in antisense therapy.

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combination therapies comprise administering an inhibitor of glycinamide ribonucleotide formyltransferase (GARFT) and/or aminoimidazolecarboximide ribonucleotide formyltransferase (AICARFT), and administering an antitoxicity agent during and after administration of the inhibitor. The combination therapies can be used for selectively killing MTAP deficient cells, and for treating cell proliferative disorders e.g. lung cancer, leukaemia, glioma, urothelial cancer, colon cancer, breast cancer, prostate cancer, pancreatic cancer skin cancer and head and neck cancer. The anti-toxicity agent counteracts the toxicity of the inhibitor in the MTAP-competent (i.e. healthy) cells and increases the maximally tolerated
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                                                                AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the present invention. N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027
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Query Best 1

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The invention relates to 971 novel human cDNA sequences (ADC29919-CC ADC30889) and the polypeptides they encode (ADC30890-ADC31860). The invention also relates to nucleic acid sequences over 99% identical with the novel human cDNAs. The invention additionally encompasses expression vectors and host cells comprising a nucleic acid of the invention; the recombinant production of a polypeptide of the invention; an antibody against a polypeptide of the invention; and methods of identifying a compound which binds to a polypeptide of the invention. The invention further discloses methods to geventing, treating or ameliorating a medical condition; kits comprising polynucleotide probes and/or monoclonal antibodies for carrying out the methods of invention; methods for the identification of compounds that modulate the expression or activity of the polynucleotide and/or polypeptide; and 767 contig sequences corresponding to the cDNA sequences of the invention (ADC33294). The nucleic acids and polypeptides of the invention are identification of mutations responsible for genetic disorders or other traits, for assessing biodiversity, and in producing many other types of data and products dependent on DNA and amino acid sequences. They are
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P-PSDB; ADC31298.
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useful
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Pred. No. 4.4e-05;
                                                                 or gene, related vectors and antibodies predisposition and treatment of cancers
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Matches 39
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                                                                                                                                                                                                                                                                                                                                                    Homo
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                                              Detecting methyl:adenosine phosphatase in mammalian cells - by hybridisation with specific oligonucleotide for detecting malignancy, also new nucleic acid, expression vectors, derived polypeptide(s) and antibodies.
                                                                                                                                                                                                                                                                                                                                                                       MTAse;
                                                                                                                                                                                                                                                                                                                                                                                         Human MTAse
                                                                                                                                                                                                                                                                                                                                                                                                           25-MAR-2003
05-DEC-1995
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                                                                                                               Nobori
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Similarity 100.0%;
39; Conservative
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d gene MTAse

library cDNA pro

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n placenta DNA MTAse genomic

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This DNA sequence comprises human genomic DNA for methylthicadenosine phosphorylase (MTase), obtained from a cosmid gene library constructed from human placenta DNA by screening with a MTase cDNA probe. A claimed method for inhibiting the activity adenylsuccinate synthetase (ASS) in mammalian cells deficient in MTAse activity involves: (a) determining

cosmid

Claim

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especially I
cancer cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                adenyl:succinate synthetase activity in methylthio:adenosine
se-deficient cells - by treatment with specific inhibitor,
L-alanosine, useful for selective killing of MTAse deficient
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ilarity 100.0%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                       lthioadenosine phosphorylase
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4.6e-05;
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Matches 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               that a population of cells obtained from a mammalian host is MTase deficient; and (b) administering an ASS inhibitor (preferably L-alanosine) to the host so that the MTase deficient host cells are depleted of AMP. The method is especially used to treat human MTAse-deficient primary tumour cells, specifically non-small cell lung cancer, acute lymphoblastic leukaemia (ALL), glioma and urothelial tumour cells. MTAse catabolises methylthioadenosine to adenine for endogenous salvage incorporation into the intracellular AMP pool. The claimed method deprives the cells of substrate for de novo synthesis of AMP, resulting in selective killing of these cells. MTAse sequence-specific oligonuclotides can be used to detect the presence or absence of MTAse in malignant cell lines
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                                                                                                                                                                                                                                                                                                              MTAse; methylthioadenosine catalytic; malignant cell;
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         Takabayashi
                                                         18-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes a novel method for detecting catalytically active and inactive methylthioadenosine phosphorylase (MTAse) in mammalian cells, using oligonucleotide probes which hybridize to MTAse nucleic acid coding regions. Detection of MTAse encoding nucleic acid indicates the cell has catalytically active MTAse encoding nucleic acid for detecting malignant cells with a deficient MTAse gene, useful for identifying malignant cells which are suitable targets for methionine (MET) starvation therapy. The new method is simple, efficient and successful at determining MTAse negative cells, unlike prior art techniques, which include analysis of catalytic activity in cell cultures, requiring a commercially unavailable radiochemical substrate, and immunoassays, using MTAse antibodies which are unable to be produced in sufficient quantities. Recombinant MTAse protein produced using the new polynucleotide and vector, allows greater and purer production of MTAse than prior art techniques (using the Rangione method) for isolating native MTAse. This sequence represents human MTAse encoding DNA which is
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                                   Inhibiting adenine succinate synthetase (ASS) activity in methylthicadenosine phosphorylase deficient cells of mammaliar involves administering ASS inhibitor which depletes adenosine monophosphate in cells.
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CDK4I;
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                                The present invention relates to novel tumour suppressor genes, termed as cyclin-dependent kinase 4 inhibitor (CDK4I) genes and their corresponding proteins. The polynucleotides are useful for preparing a composition for diagnosing or treating cancer. Sequences of the invention are also useful in gene therapy. The present sequence is human methylthioadenosine phosphorylase (MTAse) genomic DNA used in the exemplification of the invention
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                                                                                                 Antigenic peptides may be generated from this sequence encoding methyladenosine-phosphorylase, which are then used to generate antibodies specific for MTAse. The produced antibodies may be used in an immunoassay for the detection of MTase
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APPLICANT: Carson, Dennis A.
TITLE OF INVENTION: METHOD FOR SELECTITLE OF INVENTION: STARVATION OF MAI
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Louis STREET: 1880 Century Park East, Sui
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
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APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
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REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 0734
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
TELEFAX: (619) 678-5099
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local :
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TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 1:
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APPLICANT:
APPLICANT:
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LENGTH: 2763 base pairs
TYPE: nucleic acid
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REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: PD
TELECOMMUNICATION INFORMATION:
                                                                                                   FILING DATE: 0
CLASSIFICATION:
ATTORNEY/AGENT IN
                                                                                                                                                                                          ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                    SOFTWARE: Patentin
CURRENT APPLICATION D
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                   NUMBER
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ADDRESSEE: Fish & Ri
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CLASSIFICATION:
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39; Conservative
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California
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                                                                                                     INFORMATION:
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5840505ori, Tr
son, Dennis A.
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ER: PD2864
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US-08-772-113-1
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Patent No.
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Best Local (
Query Match
                                                                                                            NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: PD30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2763 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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INFORMATION F
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COMPUTER READAB
MEDIUM TYPE:
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IMMEDIATE SOURC
CLONE: methy
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                                                                                      MOLECULE T
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                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/0:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/7
FILING DATE:
CLASSIFICATION:
                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 5
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LOCATION:
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STRANDEDNESS: single
TOPOLOGY: linear
                                    LOCATION
                                                                           CLONE:
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                                                   NAME/KEY:
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                                                                                      TYPE: DI
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                                                                          methyladenosine phosphatase
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Carson, Dennis A.
Takabayashi, Kenji
TENTION: METHOD FOR DETECTION OF
JENTION: METHYLTHIOADENOSINE PHOSPHATASE
JENTION: CELLS
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                                    CDS
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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100.0%;
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Score
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Suite 500
39;
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 Length 2763;
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RESULT 6
US-08-227-800A-1
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US-09-199-137-
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APPLICATION NUMBER: US 08/176
FILING DATE: 29-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: PD30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2763 base pairs
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Matches
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GENERAL INFORMATION:
                                                                                                                          Query Match
Best Local
                                                                                                               Matches
                                                                                                                                                                                                                            TOPOLOGY: 11
MOLECULE TYPE:
IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/199,13
FILING DATE: 24-NOV-1998
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MEDIUM TYPE: Floppy disk
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Similarity 100.0%;
39; Conservative
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Application
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Cottam, F
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Conservative
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on, Dennis A
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                                                                                                             Score 39; DB 3;
Pred. No. 7.9e-06;
Mismatches 0;
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Suite 500
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hes 0;
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RESULT 7
US-08-921-954-1
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APPLICANT: Carson APPLICANT: Carson APPLICANT
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Best Local
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REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07340/023001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
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COMPUTER REA
MEDIUM TYI
COMPUTER:
OPERATING
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CITY:
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LOCATION:
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TYPE: I
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CORRESE
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CANT: NOBORI,
OF INVENTION:
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La Jolla
: California
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Similarity 100.0%;
9); Conservative 0;
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F SEQUENCES: 18
NDENCE ADDRESS:
                                                                                                                                      ICANT: Carson, Dennis A.

No. 6689864ori, Tsutomu

B OF INVENTION: Tumor Suppressor Gene a:
Detection of Cancer, Mo:
Cancer Treatment
ER OF SEQUENCES: 28
ESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Concert Townsend Concert 
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COUNTRY: USA
ZIP: 94111-3834
TER READABLE FOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Methylthioadenosine Phosphorylase (genomic)
                                                                    ITY: San Francisco
TATE: California
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                                                                                                                        REET:
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25 Executive Square, Suite
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TSUTOMU
TSUTOMU
TUMOR SUPPRESSOR GENE AND METHODS FOR DETECTION OF CANCER, MONITORING OF TUI
TREATMENT
18
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     FORM:
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Pred. No. 7.9e-06;
Mismatches 0;
                                                                                                                    Townsend and Crew LLP Center, Eighth Floor
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Monitoring of
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f Tumor
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Floppy disk

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US-08-921-954-14
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Best Local
Matches 3
                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                GENERAL INFORMATION:
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ZIP: 90012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                       NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Robbins,
STREET: 201 N. Figue
                                                                            CITY:
STATE:
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FILING DATE: 18-Jul-2001
APPLICATION NUMBER: US 08/921,954
FILING DATE: 20-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hinsch, Matthew E.
REGISTRATION NUMBER: 47,651
REFERENCE/DOCKET NUMBER: 023070-10404
REFERENCE/DOCKET NUMBER: 023070-10404
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
FOR SEQ ID NO: 14:
SECHENCE CHARACTERICS:
                                                            COUNTRY:
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LENGTH: 2763 base pa
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APPLICATION NUMBER: US/08/921,954
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                                                                          Los Angeles
California
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LOCATION:
                                                                                                                                                                                                                                              Application
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LOCATION: 1..2763
OTHER INFORMATION: /note= "full-"
methylthioadenosine phosphorylase
(MTAse) genomic nucleotide sequeno
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LOCATION: 964..1203
NCE DESCRIPTION: SEQ
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CLASSIFICATION: <Unknown>
APPLICATION DATA:
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                                                               USA
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larity 100.0%;
Conservative
                                                                                                                                                                                                                REGENTS OF THE UNIVERSITY
                                                                                                 Figueroa Street,
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616..720
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254..421
                                                                                                                                                                     METHOD FOR SELECTIVE METHIONINE STARVATION OF MALIGNANT CELLS II
                                                                                                                                                                                  METHOD
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                                                                                                                      Berliner
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5th Floor
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RESULT 9
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REFERENCE/DOCKET NUMBER: 5555
TELECOMMUNICATION INFORMATION:
TELEPHONE: 213-977-1001
TELEFAX: 213-977-1003
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2763 base pairs
TYPE: nucleic acid
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Best Local S
Matches 39
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                                          INFORMATION
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MOLECULE TYPE: DNI
MOLECULE SOURCE:
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COMPUTER READAB
MEDIUM TYPE:
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APPLICATIO
FILING DAT
CLASSIFICA
                  SEQUENCE C
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                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
FILING DATE:
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TELEPHONE
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CORRESPONDENCE ADDRESS:
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REGISTRATI
REFERENCE,
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CITY: I
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Similarity 100.0%; Pred. No. 7.9e-06; 39; Conservative 0; Mismatches 0;
Berliner, Robert
RATION NUMBER: 20,121
NCE/DOCKET NUMBER: 5555
UNICATION INFORMATION:
ONE: 213-977-1001
X: 213-977-1003
N FOR SEQ ID NO: 1:
CHARACTERISTICS:
: 2763 base pairs
nucleic acid
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WATION NUMBER: 2
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California
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     nucleic
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                                                                                                                                                                                                                                                         ADABLE FORM:
                                                                                                                                    ENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                          201 N.
                                                                                                                                                                                                                                                                                                                                         THE REGENTS OF ALL OF CALIFORNIA
OF CALIFORNIA
VENTION: METHOD FOR DETECTION OF
VENTION: METHYLTHIOADENOSINE PHOSPHATASE DEFICIENCY IN MAMMALIAN
VENTION: CELLS
                                                                                                                                                                                                                                                                                   USA
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Figueroa Street, 5th Floor
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                                                                                             5555-287
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                                                                                                                                                                                                        Version #1.25
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US-08-956-657-1
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                                                     Query Match
Best Local S
Matches 39
                                                                                                                                                                          NAME: Taylor, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 0734
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Best Loc
Matches
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GENERAL INFORMATION:

APPLICANT: No. 621001
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, V

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/956,657

FILING DATE:

CLASSIFICATION:
                                                                                                                                                                                                                                                                                   FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/

FILING DATE: 29-DEC-1993

ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Ri
                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: line MOLECULE TYPE: DI IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local 5.
                                                                                                                     TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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Similarity 100.0%;
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                                                                   Similarity
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                          AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA
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4225 Executive Square,
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larity 100.0%;
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METHOD FOR DETECTION OF
METHYLTHIOADENOSINE PHOSPHORYLASE
CELLS
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Pred.
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Pred. No. 7.9e-06;
Mismatches 0;
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Patent N GENERAL

NO.

Application 76420
MATION:

US/09335231

INFORM

APPLICANT: APPLICANT: APPLICANT:

Carson, Schmid,

Dennis A. Mathias , Carlos J.

arrera,

Sequence

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OTHER INFORMATION: exon 8 US-09-335-231-25
RESULT 12
US-09-335-231-24
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US-09-335-231-25
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SEQ ID NO 25
SEQTH: 3083
                                                                                                               Query Match
Best Local S
Matches 39
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TYPE: DNA
ORGANISM: Hon
FEATURE:
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PRIOR FILING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: genomic sequence for methylthioadenosine OTHER INFORMATION: phosphorylase (MTAP) gene NAME/KEY: modified base LOCATION: (1)..(3083)
OTHER INFORMATION: n = unknown
                                                                                                                                                                                                              NAME/KEY:
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LOCATION: (899)..(
OTHER INFORMATION:
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LOCATION: (450)
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LOCATION: (119)
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No. 6576420
INFORMATION:
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INFORMATION: exon
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INFORMATION: exon
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C: Schmid, Mathias
C: Carrera, Carlos J.
C: The Regents of the University of California
INVENTION: Method for Early Diagnosis of, and Determination
INVENTION: Prognosis in, Cancer
INVENTION: Prognosis in, Cancer
RENCE: 023070-108010US
RENCE: 023070-108010US
APPLICATION NUMBER: US/09/335,231
FILING DATE: 1999-06-17
FILING DATE: 1998-06-23
LING DATE: 1998-06-23
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nilarity 100.0%;
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                                                                                                              Score 39; DB 4;
Pred. No. 8e-06;
Mismatches
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                                                                                                                                         Length 3083;
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US-09-426-290-1/c
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; OTHER INFORMATION:
; OTHER INFORMATION:
US-09-335-231-24
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                                          Query Match
Best Local S
Matches 28
                                                                                                                                                                                                                                                                                                                                 APPLICANT: Berglind Ran Olafsdo APPLICANT: Jeffrey Gulcher TITLE OF INVENTION: HUMAN NARCO FILE REFERENCE: 2345.2001-000 CURRENT APPLICATION NUMBER: US/CURRENT FILING DATE: 1999-10-25 NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 32
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GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
                                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM:
                                                                                         LOCATION: 09-426-290-
                                                                                                                                                                                                        LOCATION:
                                                                                                                                                                                                                                                     FEATURE: NAME/KEY:
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LENGTH: 32
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                                                                                                                NAME/KEY:
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                                                                                                                                                 LOCATION:
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60300
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Vo. 6410712
INFORMATION:
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                                         Similarity 75.7%;
Similarity 75.7%;
28; Conservative
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(110324)
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ATATGGTACATTTTTCTTTTCTTTTCCAAGAAAGTA
                                                                                                                CDS
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                ATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTA
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1999-06-17
3ER: US 60/090,411
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                                                                                                   (129139)
                                                                                                                           (127130)
                                                                                                                                                  (124278)
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                                          Score 22.6; D
Pred. No. 22;
0; Mismatches
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RESULT 14 US-09-335-231-3

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US-08-592-214A-2
; Sequence 21, A
; Patent No. 581
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APPLICANT: Yanofsky, Martin r.
TITLE OF INVENTION: Cauliflower Floral Menoration of Invention: Genes and Methods of Invention of I
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Best Local S
Matches 22
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SOFTWARE: Pat
SEQ ID NO 3
LENGTH: 22
TYPE: DNA
ORGANISM: Art
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APPLICANT: Carrera, Carlos J.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Method for Early Diagnosis of, and
TITLE OF INVENTION: Prognosis in, Cancer
FILE REFERENCE: 023070-108010US
CURRENT APPLICATION NUMBER: US/09/335,231
CURRENT FILING DATE: 1999-06-17
PRIOR APPLICATION NUMBER: US 60/090,411
PRIOR FILING DATE: 1998-06-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, '

CURRENT APPLICATION DATA:
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                                                                                                                                                                   INFORMATION
                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/592
FILING DATE: 26-JAN-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
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JNICATION INFORMATION:
JNE: (619) 535-9001
K: (619) 535-8949
N FOR SEQ ID NO: 21:
CHARACTERISTICS:
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NAME/KEY: misc feature
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/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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US-09-780-114-1

US-10-326-681-25

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equence 1639, equence 7600,	ce 2445 e 1639,	quence 15 equence 1 equence 2	Sequence 13, Sequence 47, Sequence 1495	equence 256 equence 256	equence 2566 equence 2566	733 872	equence 97331,	quence 97332,	quence 219425,	quence 219425	Sequence 150817, Sequence 150817,	quence 3, Ap	quence 1, Ap	quence 123023	equenc	equence 12302	equence 123022	equence 25. Ap	nce 54, A	Sequence 31882, A	1882,

## **ALIGNMENTS**

RESULT 1 US-09-969-034-3235/c

Sequence 3235, Application No. US206 GENERAL INFORMATION:

Application US/09969034 US20040110668A1

APPLICANT:

Burgess, Christopher
Astle, Jon H.
Carroll, Eddie III
Catino, Theodore J.
Dwivedi, Poornima
Molino, Gary A.
Thiagalingam, Aruntha
Lewis, Marcia

APPLICANT:

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Sequence 3235, Ap
Sequence 1, Appli
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Sequence 2, Appli
Sequence 14, Appli
Sequence 1, Appli
Sequence 25, Appli
Sequence 24, Appl
Sequence 29328, A
Sequence 29329, A
Sequence 29329, A
Sequence 29329, A
                                                                                                                                     APPLICANT: Catino, Theodore J.
APPLICANT: Dwivedi, Poornima
APPLICANT: Molino, Gary A.
APPLICANT: Molino, Gary A.
APPLICANT: Thiagalingam, Arunthathi
APPLICANT: Lewis, Marcia E.
TITLE OF INVENTION: Nucleic Acid Sequences Differentially
TITLE OF INVENTION: Expressed in Cancer Tissue
FILE REFERENCE: 1657/1032
CURRENT APPLICATION NUMBER: US/09/969,034
CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/237,271
PRIOR FILING DATE: 2000-02-10
NUMBER OF SEQ ID NOS: 4494
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3235
LENGTH: 603
TYPE: DNA
ORGANISM: Homo sapiens
     Query N
Best Lo
Matcher
                                                                                 FEATURE:

NAME/KEY: misc_feature

LOCATION: 492, 497, 506, 527, 542,

OTHER INFORMATION: n = A,T,C or G

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   100.0%;
Similarity 100.0%;
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     Score 39; DB 11;
Pred. No. 7.3e-05;
Mismatches 0;
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APPLICANT: Boritzki, Theodore J.
APPLICANT: Ogden, Richard
APPLICANT: Ogden, Richard
APPLICANT: Skalitzky, Donald
TITLE OF INVENTION: Combination Thera
TITLE OF INVENTION: Phosphorylase De
FILE REFERENCE: PC19080A (AG110-01)
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Publication No. US20040043959A1
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                                                                                                                                                         PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR FILING DATE: 1999-11-03
                                                                         ORGANISM: Homo
10-106-698-749
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                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US
CURRENT FILING DATE: 2002-03-
                                                                                                                                                                                                                                                                       APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/1 CURRENT FILING DATE: 2003-02-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                            REFERENCE: PA005P1
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1437
                       . Similarity 39; Conser
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                                                                                                                                    PatentIn Ver.
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AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA
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DS20030109690A1
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Conservative (
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Pei-Pei
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                       100.0%;
cy 100.0%;
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Pred. No.
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Pred.
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RESULT 5
US-09-908-671-14
; Sequence 14, Ap;
; Publication No.;
; GENERAL INFOR
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; ORGANISM: Hom
US-10-779-476-2
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Best Local
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PRIOR FILING DATE: 2003-02-14
PRIOR APPLICATION NUMBER: 60/460,715
PRIOR FILING DATE: 2004-04-04
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Leoni, Lorenzo M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION AND TREATMENT
TITLE OF INVENTION: METHYLTHIOADENOSINE PHOSPHORYLASE DEFICIENT CANCERS
FILE REFERENCE: 076936-0307942
FILE REPLICATION NUMBER: US/10/779,476
CURRENT APPLICATION NUMBER: US/10/779,476
CURRENT FILING DATE: 2004-02-13
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APPLICANT: Leoni, Lorenzo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/908,671
FILING DATE: 18-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/227,800
FILING DATE: 14-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: HOWELLS, STACY L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07340/0230
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
                                                                                                                                                                                                                                  ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, V

CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, St
CITY: La Jolla
STATE: California
COUNTRY: US
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.larity 100.0%;
Conservative 0
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NOBORI, TSUTOMU
INVENTION: TUMOR SU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TUMOR SUPPRESSOR GENE AND METHODS I DETECTION OF CANCER, MONITORING OF TREATMENT
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Pred. No. 0.0001;
Mismatches 0,
                                                        07340/023001
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RESULT 6
US-09-780-114-1
; Sequence 1, Application Us,;
; Patent No. US20020146695A1
; PATERAL INFORMATION:
CENERAL TOANT: No. US200;
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                         INFORMATION
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                                                                                                                  ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vei
CURRENT APPLICATION NUMBER: US/09/780,114
FILING DATE: 09-Feb-2001
CLASSIFICATION VUMBER: US/09/072,914
FILING DATE: 04-May-1998
APPLICATION NUMBER: US 08/176,855
FILING DATE: 29-DEC-1993
APPLICATION NUMBER: US 08/459,343
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 08/827,342
FILING DATE: 26-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Bastian Kavin I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsen
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LOCATION: 1..27
SEQUENCE DESCRIPTION:
SEQUENCE CHA
LENGTH:
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LENGTH: 2763 base pa
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Similarity 100.0%;
39; Conservative (
     TELEFAX: (415) 576-
ON FOR SEQ ID NO: 1:
JENCE CHARACTERISTICS
                                NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-103030US
COMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
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CITY: Si
STATE: (
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STRANDEDNESS: single
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Takabayashi, Kenji
VENTION: Method for
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(MTAse) in a
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ne Phosphorylase
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APPLICANT: Schmid, Mathias;
APPLICANT: Carrera, Carlos J.
APPLICANT: The Regents of the University of California;
TITLE OF INVENTION: Method for Early Diagnosis of, and Det.
TITLE OF INVENTION: Prognosis in, Cancer;
FILE REFERENCE: 023070-108010US;
CURRENT APPLICATION NUMBER: US/10/326,681;
CURRENT FILING DATE: 2003-04-15;
PRIOR APPLICATION NUMBER: US 60/090,411;
PRIOR FILING DATE: 1998-06-23;
NUMBER OF SEQ ID NOS: 25
                                                                                                                                                                                                                               RESULT 7
US-10-326-681-25
                                                                                                                                                                                                                                                                                                                                                                                      ;
US-09-780-114-1
                                                                                                                                                                                  Publication No.
GENERAL INFORMA
SOFTWARE:
SEQ ID NO 2
LENGTH: 3
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Best Loc
Matches
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                                                                                                                                                                                           INFORMATION:
                                                                                                                                                                                                                                                                                                                                      39;
                         PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
CULE TYPE: DNA (genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: exon
LOCATION: 2426..2548
OTHER INFORMATION: /1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: exon
LOCATION: 1764..1953
OTHER INFORMATION: /
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RE:
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THER INFORMATION: /:
CE DESCRIPTION: SEQ
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OCATION: 724..782
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)CATION: 1378..1480
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CCATION: 899..1066
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CCATION: 119..151
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Pred. No. 0.00011;
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RESULT 8
US-10-326-681-24/c
                                                                            APPLICANT: Schmid, Mathias;
APPLICANT: Carrera, Carlos J.
APPLICANT: The Regents of the University of
ITITLE OF INVENTION: Method for Early Diagnos;
TITLE OF INVENTION: Prognosis in, Cancer
FILE REFERENCE: 023070-108010US
CURRENT APPLICATION NUMBER: US/10/326,681
CURRENT FILING DATE: 2003-04-15
PRIOR APPLICATION NUMBER: US 60/090,411
PRIOR FILING DATE: 1998-06-23
NUMBER OF SEQ ID NOS: 25
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SOFTWARE: Far
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                                                             ID NOS: 25
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US-10-027-632-29329/c
; Sequence 29329, Application US/10027632
; Publication No. US20020198371A1
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OTHER INFOR
S-10-326-681-2
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                       GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Polymorphisms in the Human Genome
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LENT APPLICATION NUMBER: US/10/027,632
LENT FILING DATE: 2002-04-30

R APPLICATION NUMBER: US 60/218,006

R FILING DATE: 2000-07-12

R APPLICATION NUMBER: US 60/198,676

R FILING DATE: 2000-04-20

R APPLICATION NUMBER: US 60/193,483

DR FILING DATE: 2000-03-29

DR APPLICATION NUMBER: US 60/185,218

DR APPLICATION NUMBER: US 60/185,218

DR APPLICATION NUMBER: US 60/167,363

DR FILING DATE: 1999-11-23

DR APPLICATION NUMBER: US 60/156,358

OR FILING DATE: 1999-09-28

OR FILING DATE: 1999-09-28
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Pred. No. 0.016;
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60/193,483

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RESULT
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          RESULT 12
US-10-027-632-29329/c; Sequence 29329, App.; Publication No. US2
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PRIOR APPLICATION NUMBER: US 60
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows V.
SEQ ID NO 29329
LENGTH: 678
                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR APPLICATION NUMBER: US 60/167,363
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LENGTH: 6
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Sequence 29328, Application US/10027632
Publication No. US20030204075A9
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TITLE OF INVENTION: Identification
TITLE OF INVENTION: Polymorphisms
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0-027-632-29329
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INFORMATION:
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mappi
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/166,358
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
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US-10-027-632-31
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                                                                    ORGANISM: Human
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RENT FILING DATE: 2002-04-30
R APPLICATION NUMBER: US 60/218,006
DR FILING DATE: 2000-07-12
PR APPLICATION NUMBER: US 60/198,676
PR FILING DATE: 2000-04-20
PR APPLICATION NUMBER: US 60/193,483
PR FILING DATE: 2000-03-29
PR APPLICATION NUMBER: US 60/185,218
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INVENTION: Identification
INVENTION: Polymorphisms
RENCE: 108827.129
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61.5%;
Similarity 84.4%;
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CATION NUMBER: US 60/185,218
G DATE: 2000-02-24
CATION NUMBER: TO THE CATION NUMBER: TO THE CATION NUMBER
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TION NUMBER: US (
DATE: 1999-09-28
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Score 24; DB Pred. No. 40; 0; Mismatches
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Pred. No. 38;
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR APPLICATION NUMBER: US 60/185,318

PRIOR APPLICATION NUMBER: US 60/185,358

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR FILING DATE: 1999-01-28

PRIOR APPLICATION NUMBER: US 60/146,002
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US-10-076-7
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US-10-027-632-31882/c
; Sequence 31882, Application US/10027632
; Publication No. US20030204075A9
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NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for W
SEQ ID NO 31882
LENGTH: 808
                                                                  APPLICANT: Karra, Kalpana
APPLICANT: Cafferkey, Robert
APPLICANT: Liu, Yongming
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Marithmeter of Invention NUMBER: US/10/076, CURRENT APPLICATION NUMBER: US/10/076, CURRENT FILING DATE: 2002-02-13
PRIOR APPLICATION NUMBER: 60/268,290
PRIOR FILING DATE: 2001-02-13
PRIOR APPLICATION NUMBER: 60/268,834
PRIOR FILING DATE: 2001-02-15
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NUMBER OF SEQ ID NOS: 129
SOFTWARE: PatentIn version
SEQ ID NO 54
LENGTH: 554
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OS: 325720
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; TYPE: DNA ; ORGANISM: Homo sapien US-10-076-747-54

Query Match 59.0%; Score 23; DB 15; Length 554; Best Local Similarity 83.9%; Pred. No. 87; Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps

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Search completed: February 1, 2005, 17:20:32 Job time : 54.6349 secs

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National Cancer Institute, Cancer Genome And
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.
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cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Sequencing by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1521 Std Error: 0.00

Seq primer: -40UP from Gibco
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Tumor Gene Index
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                 /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2188489"
/tissue_type="poorly differentiated adenocarcinoma with
signet ring cell features"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Gas4"
/note="Organ: stomach; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.69 kb. Life Technologies catalog #:
11549-011"
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1 (bases 1 to 358)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                   Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=PM4-FT0023-020
600-001-d09&t3=2000-06-02&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
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High quality sequence start: 18
High quality sequence stop: 358
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Fax: +55-11-2707001
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Proc. Natl. Acad.
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Location/Qualifiers
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_xref="taxon:9606"
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one_lib="FT0023"
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Contact: Rob
Email: cgapb
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Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisei,G., Geis
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National Cancer Institute, Cancer Genome Anat
Tumor Gene Index
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Mammalia; Eutheria;
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Wd19e10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2328618 3' similar to SW:MTAP_HUMAN_Q13126
5'-METHYLTHIOADENOSINE PHOSPHORYLASE;, mRNA sequence.
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1: cgapbs-r@mail.nih.gov
3 clone is available royalty-free through LLNL ;
3E Consortium (info@image.llnl.gov) for further ;
3primer: -40UP from Gibco.
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/clone_lib="Soares_NFL_T_GBC_S1"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NbHL19W, testis NHT, and B-cell
NCI_CGAP_GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo. "
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xref="taxon:9606"
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Primates; Catarrhini; Hominidae;
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DEFINITION
ACCESSION
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CO586973/c
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AUTHORS
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Best Local S
Matches 39
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Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; co
IMAGE Consortium (info@image.llnl.gov) for further inf
Possible reversed clone: similarity on wrong strand
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 289.
Location/Qualifiers
                                                                                                                                                                                                                                            1 (bases 1 to 568)
Schlueter, T., Hermanns, J.
Henrich, J. and Loebbert, R
Dog arrayTAG cDNA clone coupublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                            CO586973
DG2-139111
CO586973
CO586973.1
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                                                                                                                          Waldhoferstrasse 98, D-69123 Heidelberg
Tel: +49 6221 4038 150
Fax: +49 6221 4038 290
Email: Thomas.Schlueter@lionbioscience
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                           Canis familiaris (dog)
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Ve
Mammalia; Eutheria; Carnivora; Fissipedia;
                                                                                                                                                                                                                                                                                                                                                                                               EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Tel: 314 286 1800
                                                                                                                                                                                                            Contact: Thomas Schlueter LION bioscience AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity 100.0%;
Similarity 100.0%;
9; Conservative (
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/db_xref="taxon:9606"
/clone="IMAGE:1031274"
/sex="male"
                                             /organism="Canis famil
/mol_type="mRNA"
/strain="Beagle"
/db_xref="taxon:9615"
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/note="Vector: pT7T3D-Pac (Pharmacia) with
/note="Vector: pT7T3D-Pac (Pharmacia) with
polylinker; Site_1: Not I; Site_2: Eco RI;
was prepared from mRNA obtained from Clonte
Laboratories, Inc., and primed with a Not
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tissue_type="brain"
dev_stage="adult"
lab_host="DH108"
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Pred. No. 0.0016;
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s familiaris
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ia; Canidae;
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and cloned into the
pT7T3 vector. Libralization to Cot5, and
                                                                                                                                                                                                Germany
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a Not I -
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                                                                                                                                                                                                                                                                                              Kranz, H
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CD364939.
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Homo sapi
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Mammalia; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of
cDNA Library Arrayed by: Dr. M. Bento Soares, University of I
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cgap.html
Seq primer: M13 FORWARD
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project
Tumor Gene Index
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UI-H-FT2-bjn-i-17-0-UI.81 NCI CGAP FT2 Homo sapiens cDNA clone
UI-H-FT2-bjn-i-17-0-UI 3', mRNA sequence.
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Similarity 100.0%;
9; Conservative 0;
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/clone_lib="NCI_CGAP_FT2"
/clone_lib="NCI_CGAP_FT2"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI_CGAP_FT2 is a subtracted cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; pMA 10 ng/ml, 24 hours; klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Klebsiella moi 10, 3 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; wt adenovirus moi 500, 24 hours; wt adenovirus moi 500, 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours; wt adenovirus + LPS 3 hours; May vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours.
The library was subtracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
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/note="Organ: brain; Vector: Dog pBluescript LION"
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Eukaryota; Metazoa; Chorda: Mammalia; Eutheria; Primat: 1 (bases 1 to 612)
Brandenberger, R., Wei, H., Li, Y., Xu, C., Fang, R., Gue;
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DG32-195b11 DG32-1
CO701132
CO701132.1 GI:506
EST.
Canis familiaris (
Canis familiaris
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                                                                                     CN409515
17000600188932
CN409515
CN409515.1 GI:
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Mammalia; E
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Homo
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Similarity 100.0%;
39; Conservative 0
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Schlueter, T., Hermanns, J., Weindel
Henrich, J. and Loebbert, R.
Dog arrayTAG cDNA clone collection
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                           Waldhoferstrasse 98,
                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Thomas Scl
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99; Conservative (
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+49 6221 4038 150
+49 6221 4038 290
l: Thomas.Schlueter@lionbioscience
Location/Qualifiers
                                                     sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of Iowa.
TAG_TISSUE=Human Lung
TAG_LIB=UI-H-FT2
TAG_SEQ=GGCCATGCCG"
                                                                                                                                                                                                                                                                      /organism="Canis familiaris"
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/tissue_type="liver"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="DG32-liver"
/note="Organ: liver; Vector: D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Metazoa;
Eutheria;
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                                 Chordata;
Primates;
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                               Craniata; Vo
Catarrhini;
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                                           Vertebrata;
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                                           Euteleostomi;
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                                                                                                          sequence
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Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation

Nat. Biotechnol. 22 (6), 707-716 (2004)

Contact: Brandenberger R

Regenerative Medicine

Geron Corporation

230 Constitution Drive, Menlo Park, CA 94025, USA

Tel: 650 473 8658
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Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
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Length: 638 Std Error: 0.00.
Location/Qualifiers
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Length: 612 Std Error: 0.00.
Location/Qualifiers
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/tissue_type="embryonic stem cells, embryoid bodies
/tissue_type="embryonic stem cells, embryoid bodies
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/clone_lib="GRN_EB"
/note="oligo dT_primed, full-length enriched cDNA library
from embryoid body outgrowths derived from hES cell lines
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
conditions."
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/note="oligo dT_primed, full-length enriched cDNA library
from DMSO-treated hES cell line H9 (p22) maintained in
feeder-free conditions"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells,
line"
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Mammalia; Eutheria; Pri
1 (bases 1 to 681)
Kim, N.S., Hahn, Y., Oh, C
Oh, K.J., Cheong, J.E., S
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mRNA sequence.

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Plate: 32 row: F column: 01
High quality sequence stop: 681.
Location/Qualifiers
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Tel: +82-42-860-4470
Fax: +82-42-860-4409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21C Frontier Korean EST Project Unpublished (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Korea Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Kim YS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo
                                                   Similarity
9; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
Similarity 100.0%;
19; Conservative 0
AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Y.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sapiens (human)
                                                                                                                             /tissue_type="Ascites"
/cell_type="Scattering floating"
/cell_line="SNU-620"
/lab_host="Top10F'"
/clone_lib="S6SNU620"
/note="Organ: Stomach; Vector: pCNS; Site_1: EcoRI;
Site_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone="S6SNU620-32-F01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Homo sapiens
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tive 0;
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Institute of Bioscience & B:
יייאeong-gu, Daejeon 305-333,
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E., Sohn,H.Y., Kim,J.M., Park,H.S.,
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Primates;
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                                                   Score 39; I
Pred. No. 0.
; Mismatches
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Catarrhini;
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i; Hominidae;
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clone S6SNU620-32-F01 5
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3, South Korea
                                                                                  Length 681;
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Query Best L Matches

Similarity 100.0%; 39; Conservative 0

Score 39; DB 6; Pred. No. 0.0016; Mismatches 0;

Length 684;

0

Gaps

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CD364946/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
Contact: Rob
Email: cgapb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer POLYA=Yes.
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Mammalia; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cgap.html
Seq primer: M13 FORWARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST.
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I-FT2-bjn-k-07-0-UI.sl NCI_CGAP_FT2 Homo sapiens
I-FT2-bjn-k-07-0-UI 3', mRNA sequence.
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                                                                                                                                 /clone_lib=_WCI_CGAP_FT2"

/clone_lib=_WCI_CGAP_FT2"

/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI_CGAP_FT2 is a subtracted cDNA library_constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions, other donor spended for library control 0 hours; control 3 hours; control 24 hours; Rlebsiella moi 10 ng/ml, 24 hours; Rlebsiella moi 10, 3 hours; Rlebsiella moi 10, 24 hours; Staph aureus moi 10, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; wt adenovirus moi 500, 24 hours; wt adenovirus + LPS 24 hours.

The library was subtracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT2-bjn-k-07-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)
                                                                                                                           was
of 1
                   TAG_TISSUE=Human Lung Alveolar Macrophage TAG_LIB=UI-H-FT2
TAG_SEQ=GGCCATGCCG"
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Eutheria;
                                                                                                                               Iowa.
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:GAP_FT2"
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KEYWORDS
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AL048242
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Best Local
Matches 3
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TITLE
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Ma
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
 Eukaryota; Metazoa; Choro
Mammalia; Eutheria; Prima
1 (bases 1 to 836)
Ansorge, W., Wirkner, U., N
EST (Ansorge, et al.)
Unpublished (1999)
                                                                                                                                                                    AL048242

DKFZp586O1023 r1 5

DKFZp586O1023, mRN

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AL048242.1 GI:472

EST.
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BF981023
BF981023.1 GI:
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Mammalia; Eutheria;
'hages 1 to 819)
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602310222F1 NIH_MGC
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                                                                                                                                 Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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sapiens
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sapiens
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Location/Qualifiers
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larity 100.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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/clone="IMAGE:4401533"
/tissue_type="duodenal adenocarcinoma, cell line"
/tissue_t
                                                                                                                                                                                           GI:4729075
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Primates;
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Primates;
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                                             Mewes, H.W
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MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
sequenced by EMBL (European Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No s1 sequence available.
This clone (DKFZp58601023) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
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BG574734.
EST.
Homo sapi
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10572 row: k column: 18
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Location/Qualifiers
/tissue_type="mammary adenocarcinoma, cell line"
/lab_host="DH108 (phage-resistant)"
/clone_lib="NIH_MGC_87"
/note="Organ: breast; Vector: pCMV-SPORT6; Site_
Site_2: Sall; Cloned unidirectionally; oligo-dT_
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/db_xref="taxon:9606"
/clone="DKFZp58601023"
                                                                                                                           organism="Homo sapiens"

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db_xref="taxon:9606"
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/note="Vector: pSport1; Site_1: NotI; Site_
                                                                                                           clone="IMAGE:4705673"
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dev_stage="adult"
lab_host="DH10B"
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Search completed: February Job time: 439.493 secs
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E 1 (bases 1 to 900)

E Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization

Unpublished (2001)

On May 8, 2003 this sequence version replaced gi:30461423.

Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5445.f

For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSOBAG024ZA09_CS02273_1&c=5445.f
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BX390237 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI002YH04 5-PRIME, mRNA sequence.
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                                                                                                                                                                                                                                     /tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and Ecor V
sites of the pCMVSPORT 6 vector. Library was normalized.'
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/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DI002YH04"
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ALIGNMENTS

## DEFINITION ACCESSION VERSION VERSION KEYWORDS SEGMENT SOURCE ORGANISM RESULT 1 AH013410S7 LOCUS JOURNAL MEDLINE PUBMED FEATURES REFERENCE AUTHORS ORIGIN Query Ma Best Loc Matches TITLE exon source / Match 100.0%; Local Similarity 100.0%; nes 123; Conservative 0; Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 303) Nobori, T., Takabayashi, K., Tran, P., Orvis, L., Batova, A., Yu, A.L. and Carson, D.A. Genomic cloning of methylthioadenosine phosphorylase: a purine metabolic enzyme deficient in multiple different cancers Proc. Natl. Acad. Sci. U.S.A. 93 (12), 6203-6208 (1996) 96234115 Homo 7 of AH013410S7 303 bp DNA linear Homo sapiens methylthioadenosine phosphorylase (M7 L42633 L42633.1 GI:38570313 sapiens (human) /gene="MTAP" /note="putative" /number=7 Location/Qualifiers /organism="Homo sapiens" /mol\_type="genomic DNA" /db\_xref="taxon:9606" /chromosome="9" /tissue\_ 76. .198 /map="9p22-p21" /clone="cMII5" .303 \_type="placenta" Score 123; DB 9; Pred. No. 1.7e-28; ; Mismatches 0; Length 303; er PRI 01-DEC-2003 (MTAP) gene, exon 7

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Sequence 17
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Edwards, J.-B.D.M., Jobert, S. and G.
EST's and encoded human proteins
Patent: US 6639063-A 17307 28-OCT-:
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

ENCE 1 (bases 1 to 499)
HORS Edwards, J.B.D.M., Jobert, S. and Giordano, J.E.
EST and encoded human protein
Patent: JP 2002010789-A 13440 15-JAN-2002;
GENSET CORP
OS Homo sapiens (human)
PN JP 2002010789-A/13440
PD 15-JAN-2002
PF 07-AUG-2000 JP 2000280989
PR 05-AUG-2000 JP 2000280989
PR 05-AUG-1999 US 60/147499
PI JEAN BAPUTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE P
GIORDANO
PC C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact RZPD (customer.service@rzpd.de) for further informatice clone name at Harvard Institute of Proteomics (www.hip.harvard.edu): FLH131058.01L

This CDS clone is part of a collection of human full ORF cloring control of the Harvard Institute of Proteomics (HIP) and RZPD.

This CDS has been cloned without stopcodon.

The CDS has been inserted into pDONR201 via a BP Clonase (TM) reaction. Additional sequence has been added in front of the codon: att. .AAAAAA GCA GGC TCC ACC (ATG).

The last codon is followed by the 3' att site: GACCCAGCTTTCTT The clone is validated by full sequence check.

Compared to the reference sequence NM 002451 (GI:6006025) we AA exchange(s) at position (first base of changed triplet):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Heubnerweg 6, D-14
Tel: +49 30 32639
Fax: +49 30 32639
www.rzpd.de
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Contact: Inge Arlart
RZPD Deutsches Ressourcenzentru
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Submitted (28-JUN-2004) RZPD Deutsch
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Halleck,A., Ebert,L., Mkoundinya,M.,
Neubert,P., Kstrang,K., Schatten,R.,
Korn,B., Zuo,D., Hu,Y. and LaBaer,J.
Cloning of human full open reading fientry vector (pDONR201)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublishe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA exchange(s) at position (first base of changed triplet):
133(leu->ser) 166(ile->val)
Clone distribution: http://www.rzpd.de/products/orfclones/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             www.rzpd.de/cgi-bin/products/cl.c
Human Full ORF Clones Gateway(TM)
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/clone="RZPDo834H1128D"
/clone_lib="Human Full O
/lab_host="DH5Alpha"
/lab_host="DH5Alpha"
/codon_start=1
/proteIn_id="CAG46511.1"
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/db_xref="GI:49456381"
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Tel: +49 30 32639 1
Fax: +49 30 32639 1
www.rzpd.de
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                                                                             Contact RZPD (customer.service@rzpd.de) for further information. This CDS clone is part of a collection of human full ORF clones jointly established and verified by the Harvard Institute of Proteomics (HIP) and RZPD.

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Neubert,P., Kstrang,K., Schatten,R., Shen,B., Henze,S., I
Korn,B., Zuo,D., Hu,Y. and LaBaer,J.
Cloning of human full open reading frames in Gateway(TM)
entry_vector (pDONR201)
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Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg,
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Direct Submission
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Halleck, A., Ebert, L
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CDS has been inserted into pDONR201 via a ction. Additional sequence has been added into pDONR201 via a ction. Additional sequence has been added into not att. .AAAAAA GCA GGC TCC ACC (ATG). stopcodon is followed by the 3' att site: clone is validated by full sequence check.pared to the reference sequence NM_002451 (
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rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPDo834G1127D RZPDLIB;
n Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB No.
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Pred. No. 1.6e-28;
Mismatches 0;
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Shen, B., Henze,
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Sequence 1
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Combination therapies for treating methylthioadenosine phosphorylase deficient cells
Patent: WO 03074083-A 1 12-SEP-2003;
PFIZER INC. (US)
                                                                                                                                                                                                                                                synthetic construct
synthetic construct
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139(leu->met) 166(ile->val)
Clone distribution: http://www.rzpd.de/products/orfclones/.
Location/Qualifiers
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/clone="RZPDO834G1127D"
/clone_lib="Human Full ORF C
/lab_host="DH5Alpha"
/note="Vector: pDONR201, Sit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
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/brotein_id="CAG46471.1"
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/translation="MASGTTTTAVKIGIIGGTGLDDPEILEGRTEKYVDTPFGKPSDA
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QPGDIVIIDQFIDRTTMRPQSFYDGSHSCARGVCHIPMAEPFCPKTREVLIETAKKLG
LRCHSKGTMVTIEGPRFSSRAESFMFRTWGADVINMTTVPEVVLAKEAGICYASIAMA
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                                                                   /organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Cloned MTAP cDNA"
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Pred. No. 1.6e-2
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California at
GSDB:S:39613.
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and Carson,
Direct Subm
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blic enzyme deficient in multiple
Natl. Acad. Sci. U.S.A. 93 (12),
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                                                             /codon_start=1
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SVLLPRH"
                                                                                                                                                                                                                                 /gene="MTAP"
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                                                                                                                                                                                          /EC_number="2.4.
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/tissue_lib="lambda gt11"
                                                                                                                                                                                                                                                                                                               /mol_type="mxun
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Score 123; DB Pred. No. 1.5e-; Mismatches
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L. Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                      Institute, 31 Center Drive, Room 11A03, Be USA

NIH-MGC Project URL: http://mgc.nci.nih.go
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D.
cDNA Library Preparation: Michael J. Brown
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Cc
DNA Sequencing by: Institute for Systems B
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Ma
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BC026106
BC026106.1 GI:19913486
Clone distribution: MGC clone distribution through the I.M.A.G.E. Consortium/LLNL at: Series: IRAK Plate: 46 Row: h Column: 9 This clone was selected for full length sec passed the following selection criteria: maximum.
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Primates;
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                                                                                                                                                                                                                                                                                      http://mgc.nci.nih.gov
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l length sequencing because criteria: matched mRNA gi:
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Bohlander, S.K.
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HSU22233 2269 bp mRNA Human methylthioadenosine phosphorylase U22233 U22233.1 GI:847723
Olopade, O.I.
Direct Submission
Submitted (06-MAR-1995)
                                                                                                                         Construction of a 2.8-megabase yeast artificial chromosome and cloning of the human methylthicadenosine phosphorylase from the tumor suppressor region on 9p21
Proc. Natl. Acad. Sci. U.S.A. 92 (14), 6489-6493 (1995)
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ade,O.I., Pomykala,H.M., Hagos,F., Sveen,L.W., E
ade,O.I., Pomykala,H.M., Hagos,F., Sveen,L.W., E
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larity 100.0%;
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/tissue_type="Brain, hippocampus"
/clone_lib="NIH_MGC_95"
/lab_host="DH10B"
/note="Vector: pBluescript"
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/db_xref="taxon:9606"

/clone="MGC:33067 IMAGE:
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Sequence 1
AR059583
AR059583.1
                                                                                                                   1 (bases 1 to 2763)
1 (bases 1 to 2763)
Carrera, C.J., Carson, D.A., Cottam, H.B. and Nobori, T
Method for inhibiting adenylosuccinate synthetase at
methylthicadenosine phosphorylase deficient cells
patent: US 5840505-A 1 24-NOV-1998;
Location/Qualifiers
                                                                                                                                                                                                            Unknown.
Unclassified.
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Avenue, Chicago, IL 60637-1470, USA
Location/Qualifiers
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                        Similarity
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db_xref="taxon:9606"
chromosome="9"
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cell_line="primary culture"
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Pred. No. 1.5e-28;
Mismatches 0;
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Patent·
                                     1 (bases 1 to 2763)
Carson,D.A. and Nobori,T.
Tumor suppressor gene and methods for detection
monitoring of tumor progression and cancer treat
Patent: US 6689561-A 14 10-FEB-2004;
Location/Qualifiers
1. .2763
/organism="unknown"
/mol_type="genomic DNA"
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Nobori,T. and Carson,D.A.
Method for selective methionine starvation
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/organism="unknown"
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Sequence 14
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Carson,D.A. and Nobori,T.
Cyclin dependent kinase 4 inhibitor
Patent: US 6689864-A 14 10-FEB-2004;
Location/Qualifiers
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/organism="unknown"
/mol_type="genomic D
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/organism="unknown"
/mol_type="unassigned
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r suppressing multiple drug
S 6210917-A 1 03-APR-2001;
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Selectively used for tre glycinamide

y killing methylthioadenosine phosphorylase deficient cells reating cell proliferative disorders comprises administering e ribonucleotide formyltransferase and anti-toxicity agent.

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182-183;

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This invention relates to novel combination therapies that selectively kill methylthioadenosine phosphorylase (MTAP) deficient cells. The combination therapies comprise administering an inhibitor of glycinamic

glycinamide

04-MAR-2002; 09-DEC-2002;

2002US-0361645P. 2002US-0432275P.

17-FEB-2003

2003WO-IB000615.

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WO2003074083-A1.

Bloom LA, Zehnder LR,

Boritzki TJ, Kuhn LA,

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## RESULT 1 ADC37133 ID ADC37133 XX AC ADC37133; XX AC ADC37133; XX DT 18-DEC-20 XX Cloned me XX Cloned me XX Glioma; KW glycinami KW glioma; KW glioma; CO Unidentif XX DA WO2003074 XX PN WO2003074 XX PF 17-FEB-20 XX Selective PT Selective PT Used for PT Glycinami XX CC This inve CC This inve CC kill meth CC combinati combination therapy; methylthioadenosine phosphorylase; MTAP; inhibitor; glycinamide ribonucleotide formyltransferase; GARFT; aminoimidazolecarboximide ribonucleotide formyltransferase; AICARFT; anti-toxicity agent; cell proliferative disorder; lung cancer; leukaemia; glioma; urothelial cancer; colon cancer; breast cancer; prostate cancer; pancreatic cancer; skin cancer; head; neck cancer; gene; ss. Unidentified. Cloned meth ADC37133; 18-DEC-2003 8 ylthioadenosine phosphorylase, MTAP, cDNA. andard; (first entry) CDNA; 870 BP.

**ALIGNMENTS** 

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                                                                                                                                                                                                               The invention relates to 971 novel human cDNA sequences (ADC29919-CC ADC3088) and the polypoptides they encode (ADC30890-ADC31860). The invention also relates to nucleic acid sequences over 99% identical with the invention additionally encompasses expression vectors and host cells comprising a nucleic acid of the invention; the crecombinant production of a polypoptide of the invention; an antibody against a polypoptide of the invention; and methods of cidentifying a compound which binds to a polypoptide of the invention. The cidentifying a medical condition; kits comprising polynucleotide probes and/or monoclonal antibodies for carrying out the methods of the invention; methods for the identification of compounds that modulate the contist sequences corresponding to the cDNA sequences of the invention are identification of mucleic acids and polypoptide of the invention are useful in diagnostics, drug screening, forensics, gene mapping, in the customic for treating diseases such as Parkinson's diseases or also useful in disagnostics, drug screening, forensics, gene mapping, in the cancer, The nucleic acids may also be used as hybridisation polypoptides of the invention are also useful in penerating antibodies, as molecular weight markers, and in the recombinant production of a protein. They are cancer. The nucleic acids may also be used as hybridisation probes or primers, and in the recombinant production of a protein. The polypoptides are also useful in generating antibodies, as molecular weight markers, cand as food supplements. The present sequence represents a specifically to the printed specification, but was contained in electronic format directly from WIPO at
                                                                            Query Ma
Best Loc
Matches
                                                                                                                                                                                                   claimed human cDNA sequence of the invent this patent did not form part of the prin obtained in electronic format directly fr ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                             Sequence
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29-JUN-1996

(first entry)

Methylthioa denosine-phosphorylase gene.

interferon-alpha; CDK4I; tumour suppressor; chromosome-9p21; cyclin-dependent kinase-4-inhibitor; probe; primer; mutation; melanoma; diagnostic; dysplastic nevus syndrome; glioma; non-small cell lung carcinoma; cancer; gene therapy; antisense antibody; imaging; ss. methylthioadenosine-phosphorylase; chromosome walking; antisense; leukaemia;

Homo sapien

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Query Match

Best Local Similarity 100.0%;

Matches 123; Conservative (
                                                                                                                                                                                                                                                                                                                                                                               The sequence encodes a methylthioadenosine-phosphorylase, and is located at chromosome-9p21. A cyclin-dependent protein-kinase-4-inhibitor (CDK4I) tumour suppressor gene (AAT15157-58) is located between this gene and an interferon-alpha gene cluster, and has been isolated by chromosome walking. The CDK4I gene, probe and primer derivatives and the gene product may be used in diagnosis of cancer, particularly melanoma (especially dysplastic nevus syndrome), glioma, non-small cell lung carcinoma or leukaemia. The gene may also be used in cancer gene therapy, or in antitumour antisense oligonucleotide or ribozyme construction. Antibodies against CDK4I may be used in diagnosis or in vivo imaging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1995-373630/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dependent kinase inhibitor for diagnosis, assessing p
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           MTAse;
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WO9528169-A1

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Key exon

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purospnorylase (MTase), obtained from a cosmid gene library constructed from human placenta DNA by screening with a MTase cDNA probe. A claimed CC method for inhibiting the activity adenylsuccinate synthetase (ASS) in CC mammalian cells deficient in MTAse activity involves: (a) determining that a population of cells obtained from a mammalian host is MTase CC deficient; and (b) administering an ASS inhibitor (preferably L-CC alanosine) to the host so that the MTase deficient host cells are depleted of AMP. The method is especially used to treat human MTAse-CC deficient primary tumour cells, specifically non-small cell lung cancer, acute lymphoblastic leukaemia (ALL), glioma and urothelial tumour cells. MTAse catabolises methylthioadenosine to adenine for endogenous salvage in corporation into the intracellular AMP pool. The claimed method considerives the cells of substrate for de novo synthesis of AMP, resulting in selective killing of these cells. MTAse sequence-specific coligonuclotides can be used to detect the presence or ahaannous cells in malignant cell lines
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stic leukaemia; urothelial tumour
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d inactive methylthicadenosine phosphorylase (MTAse) in cells, using oligonuclectide probes which hybridize to MTAse id coding regions. Detection of MTAse encoding nucleic acid the cell has catalytically active MTAse. The method is useful ing malignant cells with a deficient MTAse gene, useful for g malignant cells which are suitable targets for methionine cration therapy. The new method is simple, efficient and lat determining MTAse negative cells, unlike prior art
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                                                                                            The present invention relates to inhibiting adenyl (ASS) activity in methylthicadenosine phosphorylase cells of mammalian host. The invention may be used cancer, especially breest and colon cancer
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CDK4I;
ds.
                The present invention relates to novel tumour suppressor genes, termed as cyclin-dependent kinase 4 inhibitor (CDK4I) genes and their corresponding proteins. The polynucleotides are useful for preparing a composition for diagnosing or treating cancer. Sequences of the invention are also useful in gene therapy. The present sequence is human methylthicadenosine phosphorylase (MTAse) genomic DNA used in the exemplification of the invention
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                                                                                                                                                                                                                         2001
                                                                                                                                                                                                                                                                                                                                                                                                                      tumour suppressor gene; cyclin-dependent kinase 4 inhibitor; cancer; gene therapy; methylthioadenosine phosphorylase; MTAse;
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                                                                                         SEQ ID NO 14; 46pp; English.
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Best Local Similarity 100.0%;

Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                    Selective methion negative tumour cells.
                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                   Antigenic peptides may be generated from this sequence encoding methyladenosine-phosphorylase, which are then used to generate specific for MTAse. The produced antibodies may be used in an if or the detection of MTase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
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Mismatches 0;
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This is the DNA sequence of a human methylthioadenosine phosphorylase C (MTAse) genomic DNA clone that was isolated from a cosmid gene library using an MTAse cDNA probe. The encoded enzyme catabolises methylthioadenosine to adenine for endogenous salvage incorporation into the intracellular AMP pool. The invention relates to methods for treating and preventing the onset and maintenance of multiple drug resistance (MDR) in animals undergoing cancer chemotherapy. In the methods provided, cells are depleted of AMP and ATP and are thus unable to supprt P-CC glycoprotein activity. One method obtains a population of target cells are treated with a purine synthesis inhibitor, such as L-alanosine, which starves the cells of adenine and suppresses P-glycoprotein activity. The Small-cell lung cancer cells, acute lymphoblastic leukemia cells, glioma cells or urothelial tumor cells, preferably in humans. MTAse competent cells are also treated for MDR with purine synthesis inhibitors. MTAse competent cells are also treated for malignancy with other anti-cancer drugs. MTase sequence-specific oligonucleotides can be used to detect the presence or absence of MTAse in malignant cell lines
                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 123
                                  Rat; methylthioadenosine | Rangione method; gene; ds
                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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04-MAY-1998
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The invention describes a method of detecting methylthioadenosine phosphorylase (MTAse) comprising adding oligonucleotide probes
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CARSON D A.
TAKABAYASHI K.
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                                                        of methylthioadenosine phosphorylase presence in mammalian adding to sample oligonucleotide probes capable of hybridizing nioadenosine phosphorylase encoding nucleic acid.
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AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decrease expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to
                                                                                                                                                                                                                                                              Nucleic
useful f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hybridisable to MTAse encoding nucleic acid to an assayable sample of cells, where the presence of the nucleic acid indicates the presence of the MTAse in a cell. The inventive method is simple and efficient in detecting the presence of MTAse in the mammalian cell. The availability of the recombinant MTAse enables the production of highly pure material with greater ease and in greater quantities than was obtained using Rangione method for the isolation and purification of native MTAse. This sequence encodes rat methylthioadenosine phosphorylase (MTAse)
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P-PSDB; AAG74252.
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03-NOV-1999;
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ABQ56306 to ABQ60787 represent isolated nucleic acids (I) differentially expressed in cancer tissues. ABB78993 to ABB79004 represent proteins encoded by the ABQ60776 to ABQ60787 nucleic acid sequences. (I) can be used in antisense therapy. An antibody immunoreactive with a polypeptide encoded by (I) is useful for detecting cancer in a patient sample, and for detecting the presence or absence of a polynucleotide encoded by a nucleic acid which hybridises to (I) in a cell. A probe/primer derived from (I) can be used for determining the presence of a nucleic acid which hybridises to (I), and for determining the phenotype of cells in a sample of cells from a patient. (I) is useful for determining the presence of colon cancer in a cell or tissue type, for determining the presence or state of other type of cancer, in antisense therapy, to generate
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                                                                                                                                                                               The present invention describes a method (M1) for screening for an anticomeoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in CC expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in CC expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's tumour
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US-09-270-767-20264
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US-09-215-681-268
US-09-216-003A-268
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RESULT 2
US-08-176-413-1
; Sequence 1, Application US/08176413
; Patent No. 5571510
; Patent No. 5571510:
; APPLICANT: No. 5571510ori, Tsutomu
; APPLICANT: Carson, Dennis A.
; TITLE OF INVENTION: METHOD FOR SELECTIVE METHIONINE
; TITLE OF INVENTION: STARVATION OF MALIGNANT CELLS IN MAMMALS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
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; LOCATION:
US-08-176-413-1
                                                                                                                                                                                             Patent No. 5840505
GENERAL INFORMATION:
APPLICANT: Carrera
APPLICANT: Cottam,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, V.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/176,413
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: PD2864
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5110
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Best Local
Matches 12
                                                                                                                                                                                                                                                 Sequence
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (σενοιμποροιαντικός)
                                                                                                                 APPLICANT: Carson, Denn.
TITLE OF INVENTION: MET!
TITLE OF INVENTION: ACT:
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0
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California
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No. 5840505ori, Tsutomu
Carson, Dennis A.
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FR: US/08/176,413
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Patent No. 594
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SEQUENCE C
LENGTH:
                                                   ZIP: 90067

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0,

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                     GENERAL
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FILING DATE: 08-MAR
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMA
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TOPOLOGY: lir
MOLECULE TYPE:
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APPLICANT:
APPLICANT:
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TELECOMMUNIC
                                                                                                                                                                                                          NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley
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SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: UFILING DATE: CLASSIFICATION: PRIOR APPLICATION DATA:
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REGISTRATI
                                                                                                                                                              STREET: 1880 Centre CITY: Los Angeles STATE: California
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                                                                                                                                                  COUNTRY:
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HONE: (619) 678-5070
AX: (619) 678-5099
ON FOR SEQ ID NO: 1:
E CHARACTERISTICS:
H: 2763 base pairs
nucleic acid
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PATION NUMBER: 34,842
                                                                                                                                                                                                                                                    INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG 1762
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                                                                                                                                                                                           1880 Century Park East, (
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                                                                                                                                                       USA
                                                                                                                                                                                                                                                   No. 5942393ori, Tsutomu Carson, Dennis A. Takabayashi, Kenji Takabayashi, Kenji TENTION: METHOD FOR DETECTION OF TENTION: METHYLTHIOADENOSINE PHOSENTION: CELLS
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Suite 500
                                                                    Version
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                                                                                                                                                                                                                                                                PHOSPHATASE DEFICIENCY IN MAMMALIAN
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RESULT 5
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                    APPLICANT: Carrera, Carlos J.
APPLICANT: Cottam, Howard B.
TITLE OF INVENTION: METHOR
TITLE OF INVENTION:
TITLE OF INVENTION:
                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, V

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/199,137

FILING DATE: 24-NOV-1998

CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (619) 455-5110 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE:
IMMEDIATE SOURCE
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REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: PD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
APPLICATION NUMBER: US (FILING DATE: 29-DEC-199)
ATTORNEY/AGENT INFORMATION
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                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 5
                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                            ADDRESSEE:
STREET: 18
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                         APPLICATION NUMBER:
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Carson, Dennis A.
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Y Park
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RESULT 6
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; LOCATION:
US-09-199-137-1
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REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: PD3(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEPAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
             TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION
REFERENCE/DOCKET NUMBER: 34,842
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
IFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTER
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MOLECULE TY
IMMEDIATE S
CLONE: m
                                                                                                CLASSIFIC ATTORNEY/AG
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SOFTWARE:
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STREET: 42
                                                                                                                        APPLICATION DATE
                                                                                                                                                                                                                                                 CITY:
STATE:
                                                                                                                                                                                                                         ZIP:
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                                                                        TORNEY/AGENT INFORMATION: NAME: HOWELLS, STACY L. REGISTRATION NUMBER: 34,
                                                                                                                                                                                    COMPUTER:
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F: NOBORI,
INVENTION:
INVENTION:
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nucleic acid
DNESS: single
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                                                                                                                                                                  READABLE FORM:

TYPE: Floppy disk

R: IBM PC compatible

NG SYSTEM: PC-DOS/MS-DOS
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California
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                                                                                                     ATE: 14-APR-1994
"ATION: 43"
                                                                                                                                  PatentIn Release
PLICATION DATA:
ION NUMBER: US/08/2
                                                                                                                                                                                                                                                                        REQUENCES: 18
RICE ADDRESS:
Fish & Richardson P.C.
4225 Executive Square, Suite
                                                                                                                                                                                                                                                                                                                                                                                                  pplication US/08227800A
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TSUTOMU
TUMOR SUPPRESSOR GENE AND METHODS FOR DETECTION OF CANCER, MONITORING OF TUR
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ER: PD3057
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                                                                                                                                                             Version
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RESULT 7
US-08-921-954-14
; Sequence 14, Application U
; Patent No. 6689864
; GENERAL INFORMATION:
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Matches
                      REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 2763 base pairs
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STRANDEDNESS: sind
TOPOLOGY: linear
MOLECULE TYPE: DNA
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LOCATION:
                                                                                                                CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/908,671A
FILING DATE: 18-Jul-2001
APPLICATION NUMBER: US 08/921,954
FILING DATE: 20-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hinsch, Matthew E.
REGISTRATION NUMBER: 47,651
                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/921,95
FILING DATE: 26-Aug-1997
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STATE: Cal
COUNTRY: U
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TYPE: nucleic STRANDEDNESS:
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ATION:
Carson, Dennis A.
No. 6689864ori, Tsutomu
No. Fumor Suppressor Gene and Detection of Cancer, Mo
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Pred. No. 2.3e-34;
Mismatches 0;
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Center, E
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LOCATION: 964..1203;
SEQUENCE DESCRIPTION: SEQUENC
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PCT-US94-14919-1
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Best Local S
Matches 123
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GENERAL INFORMATION:
                                                     INFORMATION
SEQUENCE C
                                                                                                                                                                   NAME: Berliner, Robert
REGISTRATION NUMBER: 20,121
REFERENCE/DOCKET NUMBER: 55
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Va
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 90012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: THE REGENTS OF THE UNIVERSITY
APPLICANT: OF CALIFORNIA
TITLE OF INVENTION: METHOD FOR SELECTIVE METHIONINE
TITLE OF INVENTION: STARVATION OF MALIGNANT CELLS II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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FEATURE:
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                                                   HONE: 213-977-1001

AX: 213-977-1003

ON FOR SEQ ID NO: 1:

E CHARACTERISTICS:
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California
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LOCATION: 1..2763
OTHER INFORMATION:
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2763 base pairs nucleic acid
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N. Figueroa Street, 5th Floor
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FR: 5555-286
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APPLICANT: THE REGENTS OF THE APPLICANT: OF CATTON
                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14920
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                               TELEFAX: 213-977-1003
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                         NAME: Berliner, Robert
REGISTRATION NUMBER: 20,121
REFERENCE/DOCKET NUMBER: 5555
TELECOMMUNICATION INFORMATION:
TELEPHONE: 213-977-1003
TELEFAX: 213-977-1003
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                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Robbins,
                                                    IMMEDIATE SOURCE:
                                                                  MOLECULE TYPE:
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NAME/KEY:
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                                                                (genomic)
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R: 5555-287
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Pred. No. 2.3e-34;
Mismatches 0;
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5th Floor
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US-08-956-657-1
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Best
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                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Va
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,657
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/827,342
                                                                                                                                                                             INFORMATION
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TITLE OF INVENTION: METI
TITLE OF INVENTION: METI
TITLE OF INVENTION: CELI
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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PRIOR APPLI
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                                                                                                                                                                                                                                           NAME: Tay
REGISTRAT:
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TORNEY/AGENT INFORMATION:
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                                                                                                                                         TYPE:
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                                                                                                    ENCE/DOCKET NUMBER: 34,842

MUNICATION INFORMATION:

MONE: 619/678-5070

IX: 619/678-5099

IN FOR SEQ ID NO: 1:

CHARACTERISTICS:

3083 base pairs

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EDNESS: single

3Y: linear
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Similarity 100.0%;
%3; Conservative 0
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5 Executive Square, Suite
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ON: METHOD FOR DETECTION OF
ON: METHYLTHIOADENOSINE PHOSPHORYLASE DEFICIENCY IN MAMMOLIAN
ON: CELLS
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                                                 Score 123; DB 3; Pred. No. 2.3e-34; Mismatches 0;
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                                                                          Length 3083;
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SEQ ID NO 2
LENGTH: 3
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OTHER INFORMATION: exon:
NAME/KEY: exon
LOCATION: (899)..(1066)
OTHER INFORMATION: exon:
NAME/KEY: exon
LOCATION: (1378)..(1480)
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LOCATION: (2838
OTHER INFORMATI
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ORGANISM: Homo
FEATURE:
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LOCATION: (2426)..
OTHER INFORMATION:
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LOCATION: (119)..(151)
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OTHER INFORMATION: n = unknown
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OTHER INFORMATION:
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Pred. No. 2.3e-34;
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RESULT 12
US-09-270-767-5941/c
Sequence 5941, Appl
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US-09-270-767-212
RESULT 14
US-09-235-451-
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APPLICANT: Homb...
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GENERAL
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TITLE OF INVENTION: Nucleic acids and proteins
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
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9-270-767-5941
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No. 6703491
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Similarity 57.3%;
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Sequence GENERAL 1

e 3, App

oplication ATION:

US/09235451

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APPLICANT: Caterina, Michael J.

APPLICANT: Brake, Anthony J.

TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING

TITLE OF INVENTION: CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED

TITLE OF INVENTION: CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED

CURRENT OF INVENTION: POLYPEPTIDES AND USES THEREOF

FILE REFERENCE: 9076/084CIP

CURRENT APPLICATION NUMBER: US/09/235,451

CURRENT FILING DATE: 1999-01-22

PRIOR APPLICATION NUMBER: 60/072,151

PRIOR FILING DATE: 1998-01-22

PRIOR FILING DATE: 1997-08-20

NUMBER OF SEQ ID NOS: 48

COFTWARF: FRATERO FOR Windows Version 3.0
                                                                                                                                                                                                                                                  Patent No. 6790629

GENERAL INFORMATION:
APPLICANT: Julius, David J.
APPLICANT: Caterina, Michael J.
APPLICANT: Brake, Anthony J.
TITLE OF INVENTION: Nucleic acid sequences enc.
TITLE OF INVENTION: polypeptides and uses the
FILE REFERENCE: UCALO84CON
CURRENT APPLICATION NUMBER: US/09/978,303
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/235,451
PRIOR APPLICATION NUMBER: 60/072,151
PRIOR APPLICATION NUMBER: 60/072,151
PRIOR APPLICATION NUMBER: 08/915,461
PRIOR FILING DATE: 1998-01-22
PRIOR APPLICATION NUMBER: 08/915,461
PRIOR FILING DATE: 1997-08-20
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
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ORGANISM: R.
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equence 20126	equence 2	equence 20126	equence 19727	equence 19727	equence 3, Appl	equence 9, Ap	equence 199, Ap	equence 1415, A	equence 31013	equence 31013	equence 1481	equence 17454	equence 529,	quence 72, F	equence 129,	equence 1829,	equence 1747	9 1747	equence 84, A	equence 3576,	equence 3575,	equence 36	quence 455,	equence 64								

## ALIGNMENTS

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APPLICANT: Agouron Pharmaceuticals, Inc./Pfizer Inc.;
APPLICANT: Bloom, Laura A

APPLICANT: Kuhn, Leslie
APPLICANT: Kung, Jerry Jialun
APPLICANT: Kung, Pei-Pei
APPLICANT: Zehnder, Luke
APPLICANT: Boritzki, Theodore J.
APPLICANT: Ogden, Richard
APPLICANT: Ogden, Richard
APPLICANT: Skalitzky, Donald
TITLE OF INVENTION: Combination Therapies For Treating Methylthioadenosine
TITLE OF INVENTION: Phosphorylase Deficient Cells
FILE REFERENCE: PC19080A (AG110-01)
CURRENT APPLICATION NUMBER: US/10/367,366
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 3
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US-10-3
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Best Local S
Matches 123
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                                                                                                                                             OTHER :
                                                                                                                                                                                              TYPE: DNA
ORGANISM: Artificial
                                                                                                                                                                                FEATURE:
                                                                                                                                             INFORMATION: Cloned MTAP cDNA 366-1
                                                          100.0%; Score 123; DB 16; Similarity 100.0%; Pred. No. 1.8e-31; 123; Conservative 0; Mismatches 0;
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RESULT 3
US-09-908-671-14
; Sequence 14, Application US/09908671
; Publication No. US20030138928A1
; GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 12
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CURRENT FILING DATE: 2004-02-13
PRIOR APPLICATION NUMBER: 60/447,888
PRIOR FILING DATE: 2003-02-14
PRIOR APPLICATION NUMBER: 60/460,715
PRIOR FILING DATE: 2004-04-04
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 ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopp
COMPUTER: IBM PC c
                                                                                                    NUMBER OF SEQUENCES: 18 CORRESPONDENCE ADDRESS:
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RESULT 4
US-09-780-114-1
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; Patent No. US20020146695A1
; Patent No. US20020146695
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09-908-671-14
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SEQUENC
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: Local Similarity
:hes 123; Conserv
ADDRESSEE: Townsend and Townsend an STREET: Two Embarcadero Center, Eigerty: San Francisco STATE: California COUNTRY: USA ZIP: 94111-3834
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, V
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NAME: HOWELLS, STACY L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 0734
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
ORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 2763 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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CLONE: Methylthioadenosine
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ATION: 1..2763
DESCRIPTION: SEQ
                                                                                                                                                                                                                      Takabayashi, Kenji
INVENTION: Method for Detection of the Presence or
Absence of Methylthioadenosine Phosphorylase
(MTAse) in a
                                                                                                                                                                                                                                                                                       Carson, Dennis A.
                                                                                                                                                                                                                                                                                                    US20020146695Alori,
                                                                                                                                                                                                          Cell
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                                                                                                                                                                                                         Sample
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                                                                                                                                            Townsend and Crew LLP Center, Eighth Floor
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/780, FILING DATE: 09-Feb-2001 CLASSIFICATION: <Unknown>

2545

120

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Query Ma
Best Loc
Matches
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APPLICATION NUMBER: US 08/459
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 08/827
FILING DATE: 26-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 0230
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                          Local Similarity
les 123; Conser
                                                                       Match
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                                                                                                           NAME/KEY: exon
LOCATION: 2838..2876
OTHER INFORMATION: /note=
EQUENCE DESCRIPTION: SEQ ID NO:
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LOCATION:
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LOCATION:
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LOCATION:
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APPLICATION NUMBER: US/09/072,
FILING DATE: 04-May-1998
APPLICATION NUMBER: US 08/176,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: exon
LOCATION: 119..151
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 1..3083
OTHER INFORMATION: /
phosphorylase (MTAse)
                                                                                                                                                                                                                                                                                           NAME/KEY: exon
LOCATION: 1378..1480
OTHER INFORMATION: /
                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: exon
LOCATION: 899..1066
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: exon
LOCATION: 724..782
OTHER INFORMATION:
GTTTCGGTGGACCGGGTCTTAAAGACCCCTGAAAGAAACGCTAATAAAGCCAAAAGCTTA
                                                                                                                                                                                NAME/KEY: exon
LOCATION: 2426..2548
OTHER INFORMATION: /:
                                                                                                                                                                                                                                     NAME/KEY: exon
LOCATION: 1764..195
OTHER INFORMATION:
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OTHER INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: single
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                                         Score 123; DB 9;
Pred. No. 2.6e-31;
Mismatches 0;
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RESULT 5
US-10-326-681-;
Sequence 25,
; Publication 1
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APPLICANT: Schmid, Mathias

APPLICANT: Carrera, Carlos J.

APPLICANT: The Regents of the University of California

TITLE OF INVENTION: Method for Early Diagnosis of, and Deta

TITLE OF INVENTION: Prognosis in, Cancer

FILE REFERENCE: 023070-108010US

CURRENT APPLICATION NUMBER: US/10/326,681

CURRENT FILING DATE: 2003-04-15

PRIOR APPLICATION NUMBER: US 60/090,411

PRIOR FILING DATE: 1998-06-23

NUMBER OF SEQ ID NOS: 25
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SEQ ID NO 25
LENGTH: 3083
TYPE: DNA
ORGANISM: Homo sapiens
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GENERAL INFORMATION:
A.
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NAME/KEY: exon
LOCATION: (119)..(151)
OTHER INFORMATION: exon
                                                            FEATURE:
NAME/KEY: exon
LOCATION: (2426)..(
OTHER INFORMATION:
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NAME/KEY: mod
LOCATION: (1)
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                            FEATURE:
NAME/KEY: exon
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LOCATION: (1764)..(1953)
OTHER INFORMATION: exon
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LOCATION: (724)..(782)
OTHER INFORMATION: exo
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NAME/KEY: exon
LOCATION: (450)..(536)
OTHER INFORMATION: exon
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LOCATION: (1)..(3083)
OTHER INFORMATION: n = unknown
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OTHER INFORMATION: exon
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LOCATION: (899)..(1066)
OTHER INFORMATION: exon
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ON: (2838)..(2876)
INFORMATION: exon
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RESULT
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CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: Patentin Ver. 3.0
APPLICANT: Molino, Gary A.
APPLICANT: Thiagalingam, Arunthathi
APPLICANT: Lewis, Marcia E.
TITLE OF INVENTION: Nucleic Acid Seque
TITLE OF INVENTION: Expressed in Canc
FILE REFERENCE: 1657/1032
CURRENT APPLICATION NUMBER: US/09/969,
CURRENT FILING DATE: 2001-10-02
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Best I
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LENGTH: 1437
                                                                                                                                                                                 Publication No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Local Similarity 95.0%;
les 113; Conservative
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Similarity 100.0%;
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Burgess, ...
Trile, Jon H.
                                                                                   Astle, Jon H.
Carroll, Eddie III
Catino, Theodore J.
Dwivedi, Poornima
Molino, Gary A.
Molino, Gary A.
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o. US20030109690A1
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                                          Sequences Diff
1 Cancer Tissue
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RESULT 8
                                   ; NAME/KEY: misc_feature
; LOCATION: (1)...(3186778)
; OTHER INFORMATION: n = A,
US-10-027-632-174961
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JS-09-969-034-2820
                                                                                                                                                                                                                                                                                                           APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapp.
TITLE OF INVENTION: Polymorphisms in the HI
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 174
Publication
                                                                                                                              SOFTWARE:
SEQ ID NO 1
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Best Local S
Matches 87
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LENGTH:
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LOCATION: (1)
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TYPE: DNA
ORGANISM:
FEATURE:
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ence 174961, Application US/10027632
cation No. US20020198371A1
                                                                                                                                        Match
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FILING DATE: 2000-02-10
R OF SEQ ID NOS: 4494
ARE: FastSEQ for Windows Versio
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Pred. No. 0.00099;
0; Mismatches 30;
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Score Pred.
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No. 21;
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442, 460, 466, 487, 493,
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                                                                                                Publication No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 174961
LENGTH: 3186778
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TITLE OF INVENTION: Polymorphisms in the
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
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LOCATION: (1)...(31867
OTHER INFORMATION: n =
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OR APPLICATION NUMBER: US 60/218,006

OR FILING DATE: 2000-07-12

OR APPLICATION NUMBER: US 60/198,676

OR FILING DATE: 2000-04-20

OR APPLICATION NUMBER: US 60/193,483

OR FILING DATE: 2000-03-29

OR APPLICATION NUMBER: US 60/185,218

OR APPLICATION NUMBER: US 60/185,218

OR APPLICATION NUMBER: US 60/167,363

OR APPLICATION NUMBER: US 60/156,358

OR APPLICATION NUMBER: US 60/156,358

OR APPLICATION NUMBER: US 60/146,002
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                                                                                                             3235, Application US/09969034 on No. US20040110668A1
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Similarity 58.1%;
34; Conservative
                                                           Burgess, cin-
           Astle, Jon H.
Carroll, Eddie III
Catino, Theodore J.
Dwivedi, Poornima
Molino, Gary A.
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Pred. No. 21;
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RESULT US-09-9

Sequence 21 Patent No. GENERAL INF

954-456-2116/c
954-456-2116/c
lence 2116, Application US/09954456
ent No. US20020115057A1
RAL INFORMATION:

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GENERAL INFORMATION:

APPLICANT: Augustus, Meena

TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Scr

TITLE OF INVENTION: Sets

FILE REFERENCE: 689290-70

CURRENT APPLICATION NUMBER: US/09/969,708

CURRENT FILING DATE: 2001-10-03

PRIOR APPLICATION NUMBER: US/60/237,606

PRIOR APPLICATION NUMBER: US/60/237,608

PRIOR APPLICATION NUMBER: US/60/237,608

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: US/60/237,425

PRIOR APPLICATION NUMBER: US/60/237,425

PRIOR FILING DATE: 2000-10-03
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; NAME/KEY: misc_feature
; LOCATION: 492, 497, 506, 527, 542,
; OTHER INFORMATION: n = A,T,C or G
US-09-969-034-3235
                                                                                                                             Query Match
Best Local S
Matches 43
                                                                                                                                                                                              TYPE: DNA
ORGANISM: Hom
S-09-969-708-79
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SEQ ID NO 3235
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TITLE OF INVENTION: Nucleic Acid Sequences Differentially
TITLE OF INVENTION: Expressed in Cancer Tissue
FILE REFERENCE: 1657/1032
CURRENT APPLICATION NUMBER: US/09/969,034
CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/237,271
PRIOR FILING DATE: 2000-02-10
NUMBER OF SEQ ID NOS: 4494
SOFTWARE: FastSEQ for Windows Version 4.0
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ORGANISM: Homo
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ilarity 68.3%;
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0; Mismatches
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Identifying Anti-Cancer

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RESULT 13
US-09-873-367C-646/c
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APPLICANT: Carter, Kenneth
TITLE OF INVENTION: Cancer Gene Determination
TITLE OF INVENTION: Signature Gene Sets
FILE REFERENCE: 689290-64
CURRENT APPLICATION NUMBER: US/09/873,367C
CURRENT FILING DATE: 2003-04-29
PRIOR APPLICATION NUMBER: U.S. 60/236,891
PRIOR FILING DATE: 2000-09-29
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Matches
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R APPLICATION NUMBER: US/60/235,637
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R APPLICATION NUMBER: US/60/235,638
R FILING DATE: 2000-09-26
R APPLICATION NUMBER: US/60/235,711
R APPLICATION NUMBER: US/60/235,720
R APPLICATION NUMBER: US/60/235,720
R APPLICATION NUMBER: U.S. (R FILING DATE: 2000-11-01 ER OF SEQ ID NOS: 1067 WARE: PatentIn version 3.0 D NO 646
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THE DATE: 2000-09-2
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RENT FILING DATE: 2001-10-02
OR APPLICATION NUMBER: US/60/237,172
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OR APPLICATION NUMBER: US/60/237,173
OR FILING DATE: 2000-10-02
OR APPLICATION NUMBER: US/60/237,278
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; APPLICANT: Vockley, Joseph G.
; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
; FILE REFERENCE: 44921-5026
; CURRENT APPLICATION NUMBER: US/10/240,425
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: PCT/US01/09847
; PRIOR FILING DATE: 2001-03-28
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 1588
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 363
; LENGTH: 145831
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20040033502A1 AF001548
US-10-240-425-363
Search completed: February Job time: 181.156 secs
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ALIGNMENTS

## ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 1 CD364939/c LOCUS DEFINITION REFERENCE AUTHORS TITLE JOURNAL COMMENT FEATURES source E 1 (bases 1 to 570) S NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Dr. Gary W. Hunninghake, U of I cDNA Library preparation: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/cgap.html Seq primer: M13 FORWARD POLYA=Yes. CD36 CD36 CD36 CD36 Homo Mammalia; Eutheria; Primates; Catarrhini; Hom 1 (bases 1 to 570) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anat Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 570 bp mRNA H-FT2-bjn-i-17-0-UI.sl NCI\_CGAP\_FT2 Ho H-FT2-bjn-i-17-0-UI 3', mRNA sequence. 64939.1 sapiens sapiens (human) /lab\_host="DH10B (Life Technologies)" /clone\_lib="NCI\_CGAP\_FT2" /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site\_1: EcoR I; Site\_2: Not I; NCI\_CGAP\_FT2 is a subtracted cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for lib---/clone="UI-H-FT2-bjn-i-17-0-UI" /tissue\_type="Alveolar Macrophage" /dev\_stage="Adult" /lab\_host="DH10B (Life Technologie /clone\_lib="NCI\_CGAP\_FT2" organism="Homo sapie |mol\_type="mRNA" |db\_xref="taxon:9606" ocation/Qualifiers GI:31149029 sapiens" mRNA linear EST UD-AUG FT2 Homo sapiens cDNA clone EST 05-AUG-2004 Iowa

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 612)
8 Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, (Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J and Stanton, L.W.
Transcriptome characterization elucidates signaling networks control human ES cell growth and differentiation Nat. Biotechnol. 22 (6), 707-716 (2004)
Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
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ll Similarity 100.0%;
123; Conservative (
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17000600188932 GRN_PREHEP
CN409515
CN409515.1 GI:47396639
                                                                                                                                                                                                             Email: rbrandenberger@geron.com
Insert Length: 612 Std Error:
Location/Qualifiers
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TAG_LIB=UI-H-FT2
TAG_SEQ=GGCCATGCCG"
/clone_lib="GRN_PREHEP"
/note="oligo dT_primed, full-length
from DMSO-treated hES cell line H9 |
feeder-free conditions"
                                                                                                    'mol_type="mRNA"
'db_xref="taxon:9606"
'tissue_type="embryonic
                                                                                                                                                                       organism="Homo
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Mismatches 0;
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Mammalia; Euthe:
1 (bases 1 to (
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Geron Corporation
230 Constitution Drive, Menlo Park,
Tel: 650 473 8658
Fax: 650 473 7760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J and Stanton, L.W.
Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
Contact: Brandenberger R
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Length: 638 Std Error: 0.00
Location/Qualifiers
                                                                                                                                                                                                   /tissue type="embryonic stem cells, embryoid bodies derived from H1, H7 and H9 cells"
/clone_lib="GRN_EB"
/note="oligo dT_primed, full-length enriched cDNA library from embryoid body outgrowths derived from hES cell lines H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free conditions."
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mol_type="mRNA"

db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52 Eoeun-dong Yuseong-gu, Daejeon
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 32 row: F column: 01
High quality sequence stop: 681.
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Il Similarity 100.0%;
123; Conservative 0
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Unpublished
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Mammalia; Eutheria;
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K-EST0062086
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S6SNU620-32-F01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tissue_type="Ascites"

cell_type="Scattering floating"

cell_line="SNU-620"

/lab_host="Topl0F'"

/clone_lib="S6SNU620"
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Institute of Bioscience & B:
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Primates; Catarrhini;
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                                                                                                                                                                     Score 123; DB 4; Pred. No. 7.6e-29; Mismatches 0;
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J.M., Park,H.S., Kim,
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Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniaca; vercentaca, muccare Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 684)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA Sequencing by: Dr. M. Bento Soares, Unive Clone Distribution: Distribution information http://genome.uiowa.edu/distribution/cgap.html Seq primer: M13 FORWARD
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-FT2-bjn-k-07-0-UI 3', mRNA sequence.
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                                                                                                                     /clone_lib="NCI_CGAP_FT2"

/clone_lib="NCI_CGAP_FT2"

/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI_CGAP_FT2 is a subtracted cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions, the mRNA samples were pooled for library control 24 hours; control 3 hours; Control 3 hours; Control 3 hours; Klebsiella moi 10 ng/ml, 24 hours; Staph aureus moi 10, 24 hours; Staph aureus moi 10, 24 hours; Adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; wt adenovirus moi 500, 24 hours; wt adenovirus + LPS 24 hours. The library was subtracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University
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/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologie)
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/db_xref="taxon:9606"
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Mammalia; E
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Plate: LLAM8421 row: h column: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg,
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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National Institutes of Health,
Unpublished (1999)
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3447622"
/cell_line="MGC36"
/cell_line="MGC36"
/lab_host="DH10B"
/clone_lib="NIH_MGC_10"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: Not Site_2: SalI; Cloned unidirectionally. Primer: Oligo Average insert size 1.5 kb. Library prepared by Life Technologies."
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IMAGE:3447622 5',
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Mammalia; E
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A. Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologene trios
Science 302 (5652), 1960-1963 (2003)
14671302
'L. 2017)
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Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering the body of the control of the 
                                                                                                                                                                                Homo
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DKFZp586O1023_r1 586 (synonym: DKFZp586O1023, mRNA sequence. AL048242
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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Eutheria; )
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/locus_tag="HCM2375"
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ive 0; Mismatches 0;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 975)
S NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12323 row: f column: 21
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1 Similarity 100.0%;
123; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No sl sequence available.
This clone (DKFZp586O1023) is available at the RZPD in Please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
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quality sequence stop: 636.
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/tissue_type="uterus"
/dev_stage="adult"
/lab_host="DH108"
/clone_lib="586 (synony)
/note="Vector: pSport1;
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Contact: Ge
Genoscope -
Bp 191 9100
Email: seqr
1st strand
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into the No
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Mammalia; E
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 5445.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSODE012CD01QP1&c=5445.f.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sim
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nalia; Eutheria; Primates; Catarrhini; Hominidae,
(bases 1 to 1064)
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/organism="ho....
/organism="ho....
/mol_type="mRNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="CSODE012YH01"
/tissue_type="PLACENTA"
/clone_Tib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
""As not normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sapiens (human)
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larity 100.0%;
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/db_xref="taxon:9606"
/clone="IMAGE:5574548"
/tissue_type="duodenal adenocarcinoma, cell line"
/tissue_type="MAGE:5574548"
/tissue_type="duodenal adenocarcinoma, cell line"
/clone_lib="NIH_MGC_88"
/note="Organ: small_intestine; Vector: pCMV-SPORT6;
Site_1: NotI; Site_2: SalI; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH_MGC_Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1064 b<sub>l</sub>
Homo sapiens PLACENTA
mRNA sequence.
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Pred. No. 8.1e-29;
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E 1 (bases 1 to 1380)

S Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.I.

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Schnerch, A., Schein, J.E.,

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences
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BC012316.1 GI:15147365
HTC.
               info@bcgsc.bc.
Steven Jones,
Susanna Chan,
                                                                                                                                                                                                         2 (bases 1 to 1000).
Strausberg,R.
Strausberg,R.
Direct Submission
Submitted (09-AUG-2001) National Institutes of Health, Mammalian Submitted (09-AUG-2001), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                        22388257
12477932
                                                                                           NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Genome Sequence Centre,
                                                                                                                                                                                                                                                                                                                                                                                                                                 human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A.
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gner,L., Shenmen,C.M., Schuler,G.D.,
yner,L., Schaefer,C.F., Bhat,N.K.,
wang,J., Hsieh,F.,
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                  Ran Guin,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
This clone (DKFZp686020193) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering: http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp686020193 Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.
                                                                                                                                                                                                                                   Mewes, H.W., Weil, B., Amid, C., Wiemann, S.
The German cDNA Consortium Direct Submission Submitted (13-JUL-2004) MIPS,
                                                                                                                                                                                                                                                                                                                                                                                                                  Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pass
This
                                                                                                                                            Clone from S. Wiemann, Molecular Genome Analysis, German Canc
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by EMBL (European Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of
                                                                                                                                                                                                                                                                                                                                                                                                    Homo
                                                                                                                                                                                                   Neuherberg,
Clone from
                                                                                                                                                                                                                                                                                                         Ansorge, W., Krieger, S., Re
Mewes, H.W., Weil, B., Amid,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               s clone was
sed the foll
                                                                                                                                                                                                                                                                                                                                          nryota; Metazoa; Chordata; Craniata; Vilalia; Eutheria; Primates; Catarrhini; bases 1 to 3028)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; illarity 100.0%; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTCACTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          distribution: MGC clone distribution information can be found 19th the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov 19s: IRAL Plate: 8 Row: b Column: 12 clone was selected for full length sequencing because it 19th the following selection criteria: matched mRNA gi: 6006025 clone has the following problem: frame shifted.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                   sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                sapiens (human)
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                                                                                                                             Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type- ".....9606"
/db_xref="taxon:9606"
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/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tissue_type="Placenta,
clone_Tib="NIH_MGC_21"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone="IMAGE: 3546198"
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cDNA DKFZp686020193
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                                                                                                                                                                                                                                                                                                         Regiert,T., Rittm
id,C., Osanger,A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   potb7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (from clone DKFZp686O20193).
                                                                                                                                                                                                                                                                                                                                                                                    Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                   Hominidae;
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FEATURES

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al Similarity 100.0%;
123; Conservative 0
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BF431095.1
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Clone distribution: NCI-CGAP clone distribution information found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Mammalia; Eutheria; 1 (bases 1 to 205)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trace considered overall poor
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1997)
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/db_xrer= _____/clone="IMAGE:3573-____/clone="IMAGE:3573-____/lab_host="DH10B"
/clone_lib="NCI_CGAP_Kid11"
/clone_lib="NCI_CGAP_Kid11"
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmac, label)
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmac, labe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene
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/db_xref="taxon:9606"

/clone="DKFZp686020193"

/tissue_type="esophagus tumor"

/clone_lib="686 (synonym: hlcc3). V

DH10B; sites SfiIA + SfiIB"

/dev_stage="adult"

/note="unclassified"
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/db_xref="taxon:9606"
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Primates;
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Mismatches 0;
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Local Similarity 99.2%;
les 122; Conservative
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AI91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 257)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AI919501 257 bp mRNA linear EST 14-DEC-1999 tp22b01.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2188489 3/ similar to SW:MTAP_HUMAN_Q13126 5/-METHYLTHIOADENOSINE PHOSPHORYLASE;, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria;
1 (bases 1 to 257)
                                                                                                                                                                                                                                                                                Inse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                          cDNA Library Preparation: Life Technologies, InccDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
[nsert Length: 1521 Std Error: 0.00
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                                                                                                                                                                                                                                                            primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                       1: cgapbs-r@mail.nih.gov
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/clone lib="NCI_CGAP_Gas4"
/note="Organ: stomach; Vector: pCMV-SPORT6; Site_1: Sal
Site_2: NotI; Cloned unidirectionally. Primer: Oligo of
Average insert size 1.69 kb. Life Technologies catalog
11549-011"
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                                                                                                                                                                                                                    Location/Qualifiers
                                                                                    tissue_type="poorly differentiated adenocarcinoma
signet ring cell features"
/lab_host="DH108"
                                                                                                                                                                                           'organism="Homo sapiens"
                                                                                                                                         clone="IMAGE:2188489"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GI:5639356
                                                                                                                                                      xref="taxon:9606"
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11.7

KEYWORDS SOURCE

Query Match Best Local

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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene
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                                                                                                  cell line RNA. 5 a.... follows: 5' adaptor sequence: 5'-CACGGCCATTALECC: 3' adaptor sequence: 5'-CACGGCCATTALECC: 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.5 kb (range 0.9-4.0 kb). 14/15 colonies contained inserts kb (range 1.9-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                             /db_xref="taxou:;;;;/clone="IMAGE:4668825"
/clone="IMAGE:4668825"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_60"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);
Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI
(ggccattatggcc); Double-stranded cDNA was prepared from (ggccattatggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as
                                                                                                                                                                                                                                                                                                                                                              organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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## **ALIGNMENTS**

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SM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 567)
1 (bases 1 to 567)
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2 Nobori, T., Takabayashi, K., Tran, P., Orvis, L., Batova, A., Yu, A.L.
and Carson, D.A.
Genomic cloning of methylthioadenosine phosphorylase: a purine metabolic enzyme deficient in multiple different cancers

AL Proc. Natl. Acad. Sci. U.S.A. 93 (12), 6203-6208 (1996)
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="9"
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/note="putative"
/number=6
                                                                                                                                                                                                                       /map="9p22-p21"
/clone="P1-267"
                                                                                                                                                                                        tissue_type="placenta"
4. .303
                                                                                                                                                                                                                                                                                                                     . 567
                                                             0
                                                           Score 190; DB 9;
Pred. No. 2.5e-49;
Mismatches 0;
                                                                                          Length
                                                              Indels
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                                                                                             567;
                                                              <u>.</u>
                                                           Gaps
 123
                               60
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RESULT 2
CR541710
LOCUS
DEFINITION
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AUTHORS
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AUTHORS
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    source
             This CDS has been cloned without stopcodon.
The CDS has been inserted into pDONR201 via a BP reaction. Additional sequence has been added in codon: att. .AAAAAA GCA GGC TCC ACC (ATG).
The last codon is followed by the 3' att site: Gi The clone is validated by full sequence check.
Compared to the reference sequence NM_002451 (GI AA exchange(s) at position (first base of change(133 (leu->ser) 166 (ile->val)
Clone distribution: http://www.rzpd.de/products/Clone distribution/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124
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CR541710
CR541710.1 GI:49456380
Full ORF shuttle clone, (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Halleck, A., Ebert, L., Mkound Neubert, P., Kstrang, K., Scha Korn, B., Zuo, D., Hu, Y. and L Cloning of human full open rentry vector (pDONR201)
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                                                                                                                                                                                       Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de
This clone is available from RZPD;
Contact RZPD (customer.service@rzpd.de) for further information
Clone name at Harvard Institute of Proteomics
(www.hip.harvard.edu): FLH131058.01L
This CDS clone is part of a collection of human full ORF clones
jointly established and verified by the Harvard Institute of
Proteomics (HIP) and RZPD.
This CDS has been cloned without stoncodom
                                                                                                                                                                                                                                                                                                                                                                                                                                  Germany
RZPD; RZPDo834H1128D, ORFNo 3404
www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPDo834H1128D F
Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD
Human Full ORF Clones Gateway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished

2 (bases 1 to 849)

2 (bases 1 to 849)

Halleck, A., Ebert, L., Mkoundinya, M.,
Neubert, P., Kstrang, K., Schatten, R.,
Neubert, P., Kstrang, Y., and LaBaer, J.
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                                                                                                                                                                                                                                                                                                                                                                                   RZPD Deutsches
                                                                                                                                                                                                                                                                                                                                                                                                 www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=834
www.rzpd.de/products/orfclones/
Contact: Inge Arlart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomforschung GmbH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
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1 to 849)
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Primates;
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., Schatten,R.,
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Neuenheimer Feld 580, D-69120 Heidelberg,
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                                  //www.rzpd.de/products/orfclones/
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Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                frames
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Shen, B., Henze,
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                                                                                                                                   AUTHORS
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               Genomforschung (Germany RZPD; RZPD0834G
                                                                                                                                                                                                                                                                                                                                                               stopcodon.
CR541670
CR541670.1
                                                              Halleck, A., Ebert, L., Mkoundinya, M., Neubert, P., Kstrang, K., Schatten, R., Korn, B., Zuo, D., Hu, Y. and LaBaer, J. Direct Submission
Submitted (28-JUN-2004) RZPD Deutsch
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2 (I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sim
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; RZPDo834G1127D, ORFNo 3305
rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPDo834G1127D
                                                                                                                                                bases 1 to 852)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  1670
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                                                                                                                                                                                                                                                                                                                                                                                                              sapiens full open reading frame cDNA clone RZPDo834G1127D MTAP, methylthioadenosine phosphorylase; complete cds, inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
larity 100.0%;
Conservative 0,
                                                                                                                                                                                                                                                                                                                                sapiens (human)
                                                                                                                                                                               vector (pDONR201)
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/db_xref="taxon:9606"
/clone="RZPDo834H1128D"
/clone_lib="Human Full Ol
/lab_host="DH5Alpha"
                                                                                                                                                                                                                                                                                                                                              1 GI:49456300 shuttle clone, Gateway(TM), complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MASGTTTTAVKIGIIGGTGLDDPEILEGRTEKYVDTPFGKPSDA
SILGKIKNVDCVLLARHGRQHTIMPSKVNYQANIWALKEEGCTHVIVTTACGSLREEI
QPGDIVIIDQFIDRTTMRPQSFYDGSHSCARGVCHIPMAEPFCPKTREVLIETAKKLG
LRCHSKGTMVTIEGPRFSSRAESFMFRTWGADVINMTTVPEVVLAKEAGICYASIAMA
TDYDCWKEHEEAVSVDRVLKTLKENANKAKSLLLTTIPQIGSTEWSETLHNLKNMAQF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
/protein_id="CAG46511.1"
/db_xref="GI:49456381"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="MTAP"
/codon_start
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                                               GmbH,
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Primates; Catarrhini; Hominidae;
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Pred. No. 2.5e-49;
Mismatches 0;
                                                RZPD Deutsches Ressourcenzentrum fuer
Neuenheimer Feld 580, D-69120 Heidelberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pDONR201, Site_1: attP1; Site_2:
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                                                                                                                Schick, M., Eisenstein, S., Shen, B., Henze, S., Mar, W.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Gettenbnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de
This clone is available from RZPD;
                                                                                                                                       571
                                                                                                                                                                     121
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The CDS has been inserted into pDONR201 via a BP Clonase ('reaction. Additional sequence has been added in front of codon: att. .AAAAAA GCA GGC TCC ACC (ATG).
The stopcodon is followed by the 3' att site: GACCCAGCTTT The clone is validated by full sequence check.
Compared to the reference sequence NM 002451 (GI:6006025)
AA exchange(s) at position (first base of changed triplet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact RZPD (customer.service@rzpd.de) for further information. This CDS clone is part of a collection of human full ORF clones jointly established and verified by the Harvard Institute of Proteomics (HIP) and RZPD.

This CDS has been cloned incl. stopcodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=834
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lone distribution: http://www.rzpd.de/products/orfclones/
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/mol_type="mRNA"
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/clone_lib="Human Full ORI
/lab_host="DH5Alpha"
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/codon_start=
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                                                     Submitted (09-SEP-1996) The Sam and Rose Stein Institute for Research on Aging, and Department of Medicine, University of California at San Diego, La Jolla, CA 92093-0663, USA
                                                                                                              Nobori, T., Takabay
and Carson, D.A.
Direct Submission
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sapiens methylthioadenosine phosphorylase (MTAP) mRNA,
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Carson, D.A. and Nobori, T.
Cyclin dependent kinase 4 inhibitor
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Patent: US 6689864-A 23 10-FEB-2004;
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/db_xref="taxon:9606"
/chromosome="9"
/map="9p22-p21"
/tissue_type="placenta"
/tissue_lib="lambda gt11]
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/note="putative"

/codon_start=1

/product="methylthioadenosine phosphorylase"

/protein_id="AAG38871.1"

/db_xref="GI:11602392"

/translation="MASGTTTTAVKIGIIGGTGLDDPEILEGRTEKYVDTPFGKPSDA

LILGKIKNVDCVLLARHGRQHTIMPSKVNYQANIWALKEEGCTHVIVTTACGSLREEI

QPGDIVIIDQFIDRTTMRPQSFYDGSHSCARGVCHIPMAEPFCPKTREVLIETAKKLG

LRCHSKGTMVTIEGPRFSSRAESFMFRTWGADVINMTTVPEVVLAKEAGICYASIAMG

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Pred. No. 2.4e-49;
Mismatches 0;
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Olopade, O.I.
Direct Submission
Submitted (06-MAR-1995) Olufunmilayo I. Olopaue,
University of Chicago Pritzker School of Medicine, 58
Avenue, Chicago, IL 60637-1470, USA
Location/Qualifiers
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Mammalia; Eutheria; Primates; C
1 (bases 1 to 2269)
Olopade,O.I., Pomykala,H.M., Ha
Dreyling,M.H., Gursky,S., Stadl
Bohlander,S.K.
Construction of a 2.8-megabase
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Natl. Acad. Sci. U.S.A. 92 (14), 6489-6
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LRCHSKGTMVTIEGPRFSSRAESFMFRTWGADVINMTTVPEVVLAKEAGICYASIAMA
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/cell_line="primary culture"
/cell_type="fibroblast"
/tissue_type="epidermis"
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/clone="18-11
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Carrera, C.J., Carson, D.A., Cottam, H.B. and Nobori, T.
Method for inhibiting adenylosuccinate synthetase ac
methylthicadenosine phosphorylase deficient cells
Patent: US 5840505-A 1 24-NOV-1998;
Location/Qualifiers
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Tumor suppressor gene and methods for detection of cancemonitoring of tumor progression and cancer treatment Patent: US 6689561-A 14 10-FEB-2004;
Location/Qualifiers
1. .2763
/organism="unknown"
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Location/Qualifiers
1. .2763
/organism="unknown"
/mol_type="unassigned DNA"
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1 (bases 1 to 2/05,
Carson, D.A. and Nobori, T.
Cyclin dependent kinase 4 inhibitor
Patent: US 6689864-A 14 10-FEB-2004;
Location/Qualifiers
1. .2763
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Carson,D.A. and Carrera,C.J.
Method for suppressing multiple d
Patent: US 6210917-A 1 03-APR-200
Location/Qualifiers
1. .3083
/organism="unknown"
/mol_type="unassigned DN
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/mol_type="genomic
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Mismatches 0;
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Mismatches 0;
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Laird,G.

Direct Submission
Submitted (17-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Jan 13, 2001 this sequence version replaced gi:11878000.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences wit
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alia; Eutheria; Primates;
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/mol_type="genomic"
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Mismatches 0;
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This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TEMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr9
RP11-70L8 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
This sequence is the entire insert of clone RP11-70L8 The true left end of clone RP11-14912 is at 118787 in this sequence. The true left construction/Qualifiers
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Yokota, J., Kohno, T., Inoue, K. and Kitagawa, Y.
Yokota, J., Kohno, T., Inoue, K. and Kitagawa, Y.
Direct Submission
Submitted (25-APR-2001) Takashi Kohno, National Cancer Center
Research Institute, Biology Division; 1-1, Tsukiji 5-chome,
Chuo-ku, Tokyo 104-0045, Japan (E-mail:tkkohno@gan2.res.ncc.go.jp,
Tel:81-3-3542-2511(ex.4652), Fax:81-3-3542-0807)
Location/Qualifiers
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Meng JJ;
                                                                             189pp;
                                                                                English.
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This invention relates to novel combination therapies that selectively kill methylthicadenosine phosphorylase (MTAP) deficient cells. The combination therapies comprise administering an inhibitor of glycinamide

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                                                                                                                                                                                                                                                                                                                                                                                                                        Human; diagnostic; drug screening; forensics; gene mapping; biodiversity assessment; Parkinson's disease; Alzheimer's disease; neurodegenerative diseases; anaemia; platelet disorder; wound; burns; ulcers; osteoporosis; autoimmune disease; cancer; molecular weight marker; food supplement; antiparkinsonian; nootropic; neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary; antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostatic;
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1; SEQ ID NO 409; 1185pp; English.

vectors and host cells comprising a nucleic acid of the invention; the combinant production of a polypeptide of the invention; an antibody against a polypeptide of the invention; an enthod of detecting conjunctedides or polypeptides of the invention; and methods of identifying a compound which binds to a polypeptide of the invention. The cinvention further discloses methods of peventing, treating or and/or monoclonal antibodies for carrying out the methods of the invention. The cinvention; methods for the identification of compounds that modulate the expression or activity of the polynucleotide and/or polypeptide; and 767 contig sequences corresponding to the cDNA sequences of the invention configuration of compounds that modulate the useful in diagnostics, drug screening, forensics, gene mapping, in the claritic, for assessing biodiversity, and in producing many other types of charaits, for assessing biodiversity, and an producing many other types of charaits, for assessing biodiversity, and an producing many other types of cancer. The nucleic acids may also be used as hybridisation probes or cancer. The nucleic acids may also be used as hybridisation probes or primers, and in the recombinant production of a protein. The polypeptides care also useful in generating antibodies, as molecular weight markers, cancer also applements. The present sequence represents a specifically calaimed human cDNA sequence of the invention. Note: The sequence data for obtained : ftp.wipo. and as food social The ADC this patent the nove invention e inventions inventions inventions inventions inventions inventions in the contract of the con numan cDNA sequence of the invention. Note: The sequence data for ant did not form part of the printed specification, but was in electronic format directly from WIPO at int/pub/published\_pct\_sequences. and the polypeptides they encode (ADCJV070-2007), identical with also relates to nucleic acid sequences over 99% identical with human cDNAs. The invention additionally encompasses expression human cDNAs comprising a nucleic acid of the invention; the relates to 971 novel human cDNA sequences (ADC29919-the polypeptides they encode (ADC30890-ADC31860). The

Sequence 2197 BP; 718 A; 379 C; 471 G; 629 T; 0 U; 0 Other;

Query Ma Best Loc Matches Local Match 190; Similarity Conservative 100.0%; Score 190; DB 10; 100.0%; Pred. No. 2.2e-55; ive 0; Mismatches 0; Length 2197; Indels , 0 Gaps

Ś Ş Ş 571 511 181 121 61  $\vdash$ ဂ္ဂ G Ę, 6 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG G, TCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC GGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT TTACGCAA 190 180 690 630 120 570 60

RESULT 3
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Methylthi 29-JUN-199 denosine-phosphorylase (first entry)

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05-DEC-1995
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                                                                                                                                                                                                                                                                                                                                       d gene library constructed from human placenta DNA was screened MTAse cDNA probe to isolate a human MTAse genomic clone (sequent AAQ92813). Absence of MTAse from a cell is indicative of the construction of 
                                                                                                                                                                                                                          100.0%; Score 190; DB 2; Similarity 100.0%; Pred. No. 2.4e-55; 0; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 34-35; 47pp; English.
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  GGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT
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GEIGY CORP.
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phosphorylase (MTase), obtained from a cosmid gene library constructed from human placenta DNA by screening with a MTase cDNA probe. A claimed method for inhibiting the activity adenylsuccinate synthetase (ASS) in C mammalian cells deficient in MTAse activity involves: (a) determining C deficient; and (b) administering an ASS inhibitor (preferably L-C alanosine) to the host so that the MTase deficient host cells are C depleted of AMP. The method is especially used to treat human MTAse-C actute lymphoblastic leukaemia (ALL), glioma and urothelial tumour cells. C MTAse catabolises methylthioadenosine to adenine for endogenous salvage C incorporation into the intracellular AMP pool. The claimed method constructed the cells of substrate for de novo synthesis of AMP.
                                                                                                                                                                                                                                                                                                                                                                                                              Inhibiting adenyl:succinate synthetase activity in methylthio:adenosine phosphorylase-deficient cells - by treatment with specific inhibitor, especially L-alanosine, useful for selective killing of MTAse deficient cancer cells.
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                                         24-AUG-1999
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ic; malignant cell; methionine starvation
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therapy; ss.
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RESULT 7
AAF86091
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AC AAF86091;
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DT 06-JUL-200
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DE Methylthic
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Cancer; da
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OS Unidentif:
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PN US6214571:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes a novel method for detecting catalytically active and inactive methylthioadenosine phosphorylase (MTAse) in mammalian cells, using oligonucleotide probes which hybridize to MTAse nucleic acid coding regions. Detection of MTAse encoding nucleic acid indicates the cell has catalytically active MTAse. The method is useful for detecting malignant cells with a deficient MTAse gene, useful for identifying malignant cells which are suitable targets for methionine (MET) starvation therapy. The new method is simple, efficient and successful at determining MTAse negative cells, unlike prior art techniques, which include analysis of catalytic activity in cell cultures, requiring a commercially unavailable radiochemical substrate, and immunoassays, using MTAse antibodies which are unable to be produced in sufficient quantities. Recombinant MTAse protein produced using the new polynucleotide and vector, allows greater and purer production of native MTAse. This sequence represents human MTAse encoding DNA which is used in the method of the invention
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Best Local
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                                                                                                                    Methylthioadeno cancer; ds.
                                                                                                                                                           Methylthioadenosine
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                                                                                                                                                                                                              AAF86091;
               24-NOV-1998;
                                         10-APR-2001.
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Similarity 100.0%;
90; Conservative 0
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Pred. No. 2.4e-55;
Mismatches 0;
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CDK4I;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inhibiting adenine succinate synthetase (ASS) activity in methylthicadenosine phosphorylase deficient cells of mammalian involves administering ASS inhibitor which depletes adenosine smonophosphate in cells.
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                                                                                                                                                                  tumour suppressor gene; cyclin-dependent kinase 4 inhibitor; cancer; gene therapy; methylthioadenosine phosphorylase; MTA
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22-DEC-1994;
                                WO9517908-A1
                                                                                               Enzyme; MTAase; L-Met-L-deamino-gamma-mercaptomethane
chemotherapy; cancer therapy; methionine starvation;
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il Similarity 100.0%;
190; Conservative 0
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cancer; leukaemia;

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Antigenic peptides may be generated from this sequence encoding methyladenosine-phosphorylase, which are then used to generate antibodies specific for MTAse. The produced antibodies may be used in an immunoassay for the detection of MTase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Selective methionine starvation of methyl:thio:adenosine phosphorylase negative tumour cells - used in chemotherapy of mammalian malignant cells.
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il Similarity 100.0%; Pred. No. 2.4e-55;
190; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                        2784 BP; 781 A; 505 C; 598 G; 804 T; 0 U; 96 Other;
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DNA;
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This is the DNA sequence of a human methylthioadenosine phosphorylase (MTAse) genomic DNA clone that was isolated from a cosmid gene library using an MTAse cDNA probe. The encoded enzyme catabolises methylthioadenosine to adenine for endogenous salvage incorporation into the intracellular AMP pool. The invention relates to methods for treating and preventing the onset and maintenance of multiple drug resistance (MDR) in animals undergoing cancer chemotherapy. In the methods provided, cells are depleted of AMP and ATP and are thus unable to supprt P-CC glycoprotein activity. One method obtains a population of target cells from a host and assays for loss of MTAse activity. MTAse deficient cells of adenine and suppresses P-glycoprotein activity. The Starves the cells of adenine and suppresses P-glycoprotein activity. The small-cell lung cancer cells, acute lymphoblastic leukemia cells comprising small-cell lung cancer cells, acute lymphoblastic leukemia cells, glioma cells are also treated for MDR with purine synthesis inhibitors. MTAse competent cells are also treated for MDR with purine synthesis inhibitors. MTAse competent cells are also treated for malignancy with other competent cancer drugs. MTase sequence-specific oligonucleotides can be used
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Rat; methylthioadenosine phosphorylase; MTAse; Rangione method; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG
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1481. .1763
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899. .1066
/number= 5
1764. .1953
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1067. .1377
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724. .782
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1378. .1480
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537. .723
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02-JUN-1995;
04-MAY-1998;
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TGTTACGCAA 190
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95US-00459343.
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                                                                                                                                                                                                                                                                                                                            Length 1419;
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RESULT 14
ABL81049
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                                                                                                                                                                                                                                                                                                                                                           ABQ56306 to ABQ60787 represent isolated nucleic acids (I) differentially expressed in cancer tissues. ABB78993 to ABB79004 represent proteins cencoded by the ABQ60776 to ABQ60787 nucleic acid sequences. (I) can be used in antisense therapy. An antibody immunoreactive with a polypeptide encoded by (I) is useful for detecting cancer in a patient sample, and concleic acid which hybridises to (I) in a cell. A probe/primer derived from (I) can be used for determining the presence of a nucleic acid which hybridises to (I) in a cell. A probe/primer derived from (I) can be used for determining the phenotype of cells in a sample of cells from a patient. (I) is useful for determining the presence of colon cancer in a cell or tissue type, for determining the presence or state of other type of cancer, in antisense therapy, to generate macroarrays on a solid surface, to identify a chromosome on which the corresponding gene resides, and in tissue profiling, forensics, genetic analysis, mapping and diagnostic applications. (I) can be used to raise antibodies, and to screen for peptide analogues and antagonists
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Thiaglingam
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Il Similarity 90.1%;
173; Conservative
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                                              standard;
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                                                                                                                     TTTGTTACGCAA
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                                                                                                                                                                                                                                                                                         Score 135.2; DB 6;
Pred. No. 1.6e-36;
); Mismatches 16;
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The present invention describes a composition (I) comprising: carriers and immunostimulants; and a polypeptide (II) of a ovarian tumour polypeptide encoded by a polynucleotide (III) having a cDNA sequence (S1) from the 10912 nucleotide sequences as given in ABL77023 to ABL87934, (III) encoding (II) having a sequence (S2), a T cell population of (II), cor antigen presenting cells that express (II). (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to (S1) can be used for detecting ovarian cancer in a patient's biological sample preferably serum or ovarian tissue. The method comprises contacting a biological sample from a patient with (IV), detecting the amount of polynucleotide (IV) and comparing the amount to a predetermined cutoff value and thereby detecting ovarian cancer in the patient, where the amount of polynucleotide hybridising to (IV) is detected preferably by clymerase chain reaction (PCR). (I) comprising (III) and/or (II) is useful for stimulating and/or expanding T cells specific for an ovarian cutoff cutofin design and preparation of ribozyme molecules for inhibiting contesting and preparation of ribozyme molecules for inhibiting contesting well known techniques
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                                                                                                                                                                                                                    ch 62.6%; Score 119; DB 6; Length 44
ll Similarity 100.0%; Pred. No. 6.1e-31;
119; Conservative 0; Mismatches 0; Indels
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AATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGG 119
                                                                                                                                         TCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
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                                                                                                                   TCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGGACAATGGTC 382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for therapy and diagnosis of ovarian cancer comprising of a ovarian tumor polypeptide, polynucleotide encoding, antibody specific to polypeptide or T cell expressing
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                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic a genes from Drosophila interactions.
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P-PSDB; ABB64238.
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11-JUL-2000;
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nilarity 66.7%;
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Pred. No. 1.4e-19;
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equence 106,	e 101,	Ò	e 1, Appl	Sequence 1, Appli	equence 252, F	equence 3298,	equence 3296,	equence 1498,	equence 33, A	Į	equence 9, Appl	equence 9, Appl	equence 9, App	equence 26, App	equence 26, App	equence 26, App	

## ALIGNMENTS

RESULT 1
US-08-921-954-23
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Application 89864

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INFORMATION
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/908,671A
FILING DATE: 18-Ju1-2001
APPLICATION NUMBER: US 08/921,954
FILING DATE: 20-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hinsch, Matthew E.
REGISTRATION NUMBER: 47,651
REFERENCE/DOCKET NUMBER: 023070-10404
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
TELEPAX: (415) 576-0300
TELEPAX: (415) 576-0300
                                                      LENGTH: 1450 base pair
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic
FEATURE:
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NAME/KEY:
LOCATION:
OTHER INFO
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HER INFORMATION:
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PE: nucleic acid
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ONDENCE ADDRESS:
DRESSEE: Townsend
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No. 6689864ori, Tsutomu
NVENTION: Tumor Suppressor Gene and Methods for
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                          ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: PD28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2763 base pairs
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: PATEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, V

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/176,413

FILING DATE:

CLASSIFICATION: 424
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APPLICANT:
TITLE OF IN
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn
STREET: 1880 Century Park
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STATE:
TYPE: nucleic STRANDEDNESS:
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US-08-612-542B-1
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AITON:
Carrera, Carlos J.
APPLICANT: Cottam, Howard B.
APPLICANT: No. 58405050ri, Tsutomu
APPLICANT: Carson, Dennis A.
TITLE OF INVENTION: METHOD FOR INT
TITLE OF INVENTION: ACTIVITY
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDREST
STREET: 47
CITY:
STREET: 47
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Best Local S
Matches 190
                                                                                                                                                                                                                                                                     CITY: 4225 Executive CITY: La Jolla STATE: California COUNTRY: USA ZIP: 92037
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy di COMPUTER: IBM
                                                                                              INFORMATION
                                                                                                                                                APPLICATION NUMBER: US/08/612
FILING DATE: 08-MAR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 0734
                                                                  SEQUENCE (
LENGTH:
                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
CURRENT APPLICATION DATA:
                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
TELEFAX: (619) 678-5099
FORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
MOLECULE TYPE: IMMEDIATE SOUR
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LOCATION:
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                                         STRANDEDNESS:
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                          TOPOLOGY:
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 SOURCE:
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3: DNA
                           linear
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5 Executive Square, Suite 1400
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08-MAR-1996
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TY IN MALIGNANT METHYLTHIOADENOSINE PHOSPHORYLASE DEFICI
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RESULT 4
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                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/176
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: PD30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2763 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Matches
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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APPLICANT: Carson, Denni
APPLICANT: Takabayashi,
TITLE OF INVENTION: METH
TITLE OF INVENTION: METH
TITLE OF INVENTION: CELI
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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NAME/KEY:
LOCATION:
8-612-5428-1
                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/772,
                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: 18
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                                                                                                                                                                                                                         PILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                COUNTRY: US
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California
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1880 Century Par
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Carson, Dennis A.
Takabayashi, Kenj
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METHOD FOR DETECTION OF

METHYLTHIOADENOSINE PHOSPHATASE D

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(genomic)
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Park East,
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Pred. No. 4.9e-60;
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                                                                                                                                                                                                                                                                                                                                                                                                     & Lubitz
Suite 500
                                                                                                                                                                                                                                                                                 Version
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RESULT 5
US-09-199-137-1
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                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2763 base pairs
TYPE: nucleic acid
STRANDENNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 190
                                                                                                                       FILING DATE: 29-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: PD3057
TELECOMMUNICATION
                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/199,137
FILING DATE: 24-NOV-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/176,855
APPLICATION NUMBER: US 08/176,855
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FEATURE:
NAME/KEY:
LOCATION:
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STATE: C
COUNTRY:
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           STRANDEDNESS: 811
TOPOLOGY: linear
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INFORMATION:
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IT: Carson, Dennis A.
IT: Carrera, Carlos J.
IT: Cottam, Howard B.
INVENTION: METHOD FO
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California
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1880 Century Park East, Suite 5
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1..2763
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESS:
DNA (genomic)
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US-08-227-800A-14
; Sequence 14, Ap
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Best Local S
Matches 190
                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, 1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/227,800/
FILING DATE: 14-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HOWELLS, STACY L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07340/02:
TELEPHONE: 619/678-5070
TELEPHONE: 619/678-5070
                                                                                         TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF
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TITLE OF IN
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                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: DE
TITLE OF INVENTION: TR
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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CITY: 1
                                     TYPE: nucleic acid STRANDEDNESS: sing TOPOLOGY: linear
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190; Conservative
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La Jolla
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TUMOR SUPPRESSOR GENE
DETECTION OF CANCER, M
TREATMENT
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ER: 07340/023001
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Pred. No. 4.9e-60;
Mismatches 0;
Phosphorylase
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RESULT 7
US-08-921-954-14
; Sequence 14, Ap
; Patent No. 6689
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PRIOR APPLICATION: *CONKNOWN*
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/908,671A
FILING DATE: 18-Jul-2001
APPLICATION NUMBER: US 08/921,954
FILING DATE: 20-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hinsch, Matthew E.
REGISTRATION NUMBER: 47,651
REFERENCE/DOCKET NUMBER: 023070-104042US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0200
TINFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 2763 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: -
LOCATION: 1..2763
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Matches
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STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ver
SOFTWARE: PatentIn Release #1.0, Ver
APPLICATION NUMBER: US/08/921,954
FILING DATE: 26-Aug-1997
CLASSIFICATION: <Unknown>
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No. 6689864
AL INFORMATION:
APPLICANT: Carson, Dennis A.
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il Similarity 100.0%;
190; Conservative 0;
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SPONDENCE ADDRESS:
ADDRESSEE: Townsend and
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No. 6689864ori, Tsutomu

INVENTION: Tumor Suppressor Gene and Methods

Detection of Cancer, Monitoring of Cancer Treatment
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                                                                                                                                                                                                                                                                                                                                                                                                                    #1.0, Version
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RESULT 8
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SEQUENCE DESCRIPTION: SEQUENCE DESCRIPTION: SEQUENCE DESCRIPTION: SEQUENCE DESCRIPTION: SEQUENCE
                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Vere
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14919
FILING DATE:
CLASSIFICATION:
NAME: Berliner, Robert
REGISTRATION NUMBER: 20,121
REFERENCE/DOCKET NUMBER: 555-286
TELECOMMUNICATION INFORMATION:
TELEPHONE: 213-977-1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application:
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Best Local Similarity 100.0%;
Matches 190; Conservative (
                                     TELEFAX: 213-977-1003
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 5
LENGTH: 2763 b
TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                                                                          COUNTRY: US
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CITY: 1
STATE:
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LOCATION:
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                          2763 base pairs
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Pred. No. 4.9e-60;
Mismatches 0;
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                                                                                                                                                                                                                       Version
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                                                                                    NAME: Berliner, Robert
REGISTRATION NUMBER: 20,121
REFERENCE/DOCKET NUMBER: 5555
TELECOMMUNICATION INFORMATION:
TELEPHONE: 213-977-1001
TELEFAX: 213-977-1003
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2763 base pairs
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Best Local
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14920
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Berliner, Robert
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APPLICANT:
TITLE OF IN
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IMMEDIATE SO
CLONE: me
CLONE: FEATURE:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                      TOPOLOGY: 1
MOLECULE TYPE:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Robbins,
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LOCATION:
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Similarity 100.0%; Pred. No. 4.9e-60;
90; Conservative 0; Mismatches 0;
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California
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           methyladenosine phosphatase
                         SOURCE:
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YPE: DNA
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Figueroa Street, 5th Floor
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                                                                                                         INFORMATION FOR SEQ
                                                                                                              NAME: Taylor, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 0734
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5099
TELEFAX: 619/678-5099
                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/95
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/827,3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                APPLICATION NUMBER: US 0 FILING DATE: 29-DEC-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                           ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.
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                                   LENGTH: 3083 Dage
TYPE: nucleic acid
STRANDEDNESS: sind
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I Similarity 100.0%;
190; Conservative (
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F INVENTION: CELLS
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                                                                                          CHARACTERISTICS:
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R: 07340/050001
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Suite 1400
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No. 4.9e-60;
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AMPLICANT: Carson, Dennis A.

APPLICANT: Schmid, Mathias

APPLICANT: The Regents of the University of California

TITLE OF INVENTION: Method for Early Diagnosis of, and Dete

TITLE OF INVENTION: Prognosis in, Cancer

FILE REFERENCE: 023070-108010US

CURRENT APPLICATION NUMBER: US/09/335,231

CURRENT APPLICATION NUMBER: US/09/335,231

CURRENT FILING DATE: 1999-06-17

PRIOR APPLICATION NUMBER: US 60/090,411

PRIOR FILING DATE: 1998-06-23

NUMBER OF SEQ ID NOS: 25

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 25

LENGTH: 3083

TYPE: DNA

CORGANT
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LOCATION: (450)..(536)
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LOCATION: (2426)..(
OTHER INFORMATION:
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OTHER INFO
                 NAME/KEY: ex
LOCATION: (2
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OTHER INFORMATION: genomic sequence for OTHER INFORMATION: phosphorylase (MTAP)
NAME/KEY: modified base
LOCATION: (1)..(3083)
OTHER INFORMATION: n = unknown
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LOCATION: (1
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NAME/KEY: exon
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LOCATION: (119)..(151)
OTHER INFORMATION: exon
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Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13253
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US-09-2
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US-09-103-840A-2
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Best Local S
Matches 190
                                                         Sequence 2, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
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APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
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Pred. No. 4.6e-22;
); Mismatches 62;
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Pred. No. 5.1e-60;
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; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
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US-09-103-840A-1
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; OTHER INFORMATION: "n" bases
; OTHER INFORMATION: represent
US-09-103-840A-2
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Best Local S
Matches 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRATITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
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SOFTWARE: 1
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ORGANISM: Mycobacterium tuberculosis
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Vo. 6294328
INFORMATION:
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   ACTCGAATTATGCTACGCA
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Pred. No. 1.7e-08;
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RESULT US-09-2

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Sequence 3979, Application US/09248796A;
Patent No. 6747137;
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES REL
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132;
CURRENT APPLICATION NUMBER: US/09/248,796A;
CURRENT FILING DATE: 1999-02-12;
PRIOR APPLICATION NUMBER: US 60/074,725;
PRIOR APPLICATION NUMBER: US 60/074,725;
PRIOR APPLICATION NUMBER: US 60/096,409;
PRIOR FILING DATE: 1998-02-13;
PRIOR FILING DATE: 1998-08-13;
NUMBER OF SEQ ID NOS: 28208;
SEQ ID NO 3979;
LENGTH: 738
                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-3979
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Search completed: February Job time: 67.497 secs
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Best Local Similarity 55.4%;
Matches 77; Conservative
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Pred. No. 9.1e-05;
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2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

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4: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

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6: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

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9: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

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14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

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US-09-867-701-4027

8 US-10-653-047-7072

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Sequence 6576, Ap
Sequence 53, Appl
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equence equence equence	equence 1, App equence 11, Ap quence 350, Ap equence 9, App equence 1324,	nce 100 nce 338 nce 568 nce 205	equence 3666, A Sequence 1, App quence 1002, Ap equence 1002, A	Sequence 158, Appli Sequence 7, Appli Sequence 2058, Ap Sequence 40954, A Sequence 40954, A Sequence 3336, Ap	Sequence 17, Sequence 61, Sequence 458 Sequence 142 Sequence 458 Sequence 123 Sequence 267

## ALIGNMENTS

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APPLICANT: Bloom, Laura A

APPLICANT: Kuhn, Leslie

APPLICANT: Kuhn, Leslie

APPLICANT: Meng, Jerry Jialun

APPLICANT: Meng, Jerry Jialun

APPLICANT: Cehnder, Luke

APPLICANT: Schnder, Luke

APPLICANT: Ogden, Richard

APPLICANT: Ogden, Richard

APPLICANT: Skalitzky, Donald

TITLE OF INVENTION: Combination Therapies For Treating Methylthicadenosine

TITLE OF INVENTION: Phosphorylase Deficient Cells

FILE REFERENCE: PC19080A (AG110-01)

CURRENT APPLICATION NUMBER: US/10/367,366

CURRENT FILING DATE: 2003-02-14

NUMBER OF SEQ ID NOS: 3

CODTMANDE: Detaits 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
US-10-3
                                                                                                                                                         ; FEATURE:
; OTHER INFORMATION: Cloned MTAP cDNA
US-10-367-366-1
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Best Local S
Matches 190
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SEQ ID NO 1
LENGTH: 870
TYPE: DNA
ORGANISM: Artificial
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Publication No
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APPLICANT: Agouron
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                                                                    100.0%; Score 190; DB 16; illarity 100.0%; Pred. No. 7.1e-61; Conservative 0; Mismatches 0;
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RESULT 2
US-10-779-476-2
; Sequence 2, Application US/1077947
; Publication No. US20040247600A1
; GENERAL INFORMATION:
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ORGANISM: Homo
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SEQ ID NO 2
LENGTH: 2
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CURRENT APPLICATION NUMBER: US/10/779,476

CURRENT FILING DATE: 2004-02-13

PRIOR APPLICATION NUMBER: 60/447,888

PRIOR FILING DATE: 2003-02-14

PRIOR APPLICATION NUMBER: 60/460,715

PRIOR FILING DATE: 2004-04-04

NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Salmedix, Inc.
APPLICANT: Leoni, Lorenzo M
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & 1
                                                           TITLE
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NOBORI, T
INVENTION:
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, TSUTOMU
N: TUMOR SUPPRESSOR GENE A
DETECTION OF CANCER, MC
TREATMENT
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Richardson
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Pred. No. 9.8e-61;
Mismatches 0;
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                                              MONITORING
                                             AND METHODS I
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STREET: ".
CITY: La JOL.
STATE: Californi.
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Vers;
APPLICATION NUMBER: US/09/908,671
FILING DATE: 18-Jul-2001
CLASSIFICATION LOATA:
APPLICATION NUMBER: US/08/227,800
FILING DATE: 14-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: HOWELLS, STACY L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07340/(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEPHONE: 619/678-5070
TELEFAX: 619/678-509
'ATTON FOR SEQ ID NO: 14:
"MCE CHARACTERISTICS:
"TH: 2763 base pairs
"ucleic acid
"S: single
"ATTON STATE TO TOMIC)
"TELEPHONE STATE TOMICS TO
                                                                                                                -806-60-Sn
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Best Local
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: Methylthioadenosin
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   NUMBER
                                                                                           TITLE
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LOCATION:
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                                                                                           OF.
   မ္ပ
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Takabayashi, Kenji
F INVENTION: Method for Det
Absence of Met
(MTAse) in a
Cell Sample by
OF SEQUENCES: 1
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larity 100.0%; Pred. No. 1e-60;
Conservative 0; Mismatches
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ATION: 1..2763
DESCRIPTION: SEQ
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                                                                    Detection of the Presence or Methylthioadenosine Phosphorylase
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                           Presence
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INFORMATION FOR SEQ ID NO:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,914
FILING DATE: 04-May-1998
APPLICATION NUMBER: US 08/176,855
FILING DATE: 29-DEC-1993
APPLICATION NUMBER: US 08/459,343
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 08/827,342
FILING DATE: 26-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REGISTRATION NUMBER: 34,774
                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: exon
LOCATION: 119..151
OTHER INFORMATION:
FEATURE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/780,114
FILING DATE: 09-Feb-2001
CLASSIFTCATTON
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FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Townsen
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TOPOLOGY: linea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: COMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200 TELEFAX: (415) 576-0300
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STATE: Cal
                                                                                                                                            NAME/KEY:
                                                                                                                                                                                           NAME/KEY: exon
LOCATION: 899..1066
OTHER INFORMATION:
                                                                                                                                                                                                                                                         NAME/KEY: exon
LOCATION: 724..782
OTHER INFORMATION:
NAME/KEY: exon
LOCATION: 2426..2548
OTHER INFORMATION: /:
                                                             NAME/KEY: exon
LOCATION: 1764..1953
OTHER INFORMATION: /
                                                                                                                            NAME/KEY: exon
LOCATION: 1378..1480
OTHER INFORMATION: /
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LOCATION: 450..536
OTHER INFORMATION:
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OTHER INFORMATION:
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LENGTH: 3083 base pa
                              NAME/KEY:
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APPLICANT: Carson, Dennis A.

APPLICANT: Schmid, Mathias

APPLICANT: Carrera, Carlos J.

APPLICANT: The Regents of the University of California

TITLE OF INVENTION: Method for Early Diagnosis of, and Dete

TITLE OF INVENTION: Prognosis in, Cancer

FILE REFERENCE: 023070-108010US

CURRENT APPLICATION NUMBER: US/10/326,681

CURRENT FILING DATE: 2003-04-15

PRIOR APPLICATION NUMBER: US 60/090,411

PRIOR FILING DATE: 1998-06-23

NUMBER OF SEQ ID NOS: 25

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 25
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Best L
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                                                                                                                                                                                                                                                                                                    FEATURE:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                  NAME/KEY: exon
LOCATION: (450)..(536)
OTHER INFORMATION: exo
                                                                                                                                                                            FEATURE:
NAME/KEY: exon
LOCATION: (119)..(151)
OTHER INFORMATION: exon
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LOCATION: (1)..(3083)
OTHER INFORMATION: n = u
                                                         LOCATION: (724)..(782)
OTHER INFORMATION: exo
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LOCATION: 2838..2876
OTHER INFORMATION: /note= "exon
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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            (899) . . (1066)
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ATION:
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                                                                                                                                                                                                                                                                                                   genomic sequence for methylthioadenosine phosphorylase (MTAP) gene
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exon
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100.0%; Pred. No. 1.1e-60;
tive 0; Mismatches 0;
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APPLICANT: Dwivedi, Poornima
APPLICANT: Molino, Gary A.
APPLICANT: Thiagalingam, Arunthathi
APPLICANT: Lewis, Marcia E.
TITLE OF INVENTION: Nucleic Acid Sequences Differentially
TITLE OF INVENTION: Expressed in Cancer Tissue
FILE REFERENCE: 1657/1032
CURRENT APPLICATION NUMBER: US/09/969,034
CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/237,271
PRIOR FILING DATE: 2000-02-10
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Best Local S
Matches 190
                                                                                                                                                                                                                                                                                                                                      Publication No. US20 GENERAL INFORMATION:
                                                                                                                      SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                    NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
EQ ID NO 2820
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          FEATURE:
NAME/KEY: I
LOCATION:
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NAME/KEY:
LOCATION:
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LOCATION: (2426)..
OTHER INFORMATION:
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LOCATION: (1764)..
OTHER INFORMATION:
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LOCATION: (1378)..
OTHER INFORMATION:
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NAME/KEY: exon
                                                                                    ORGANISM:
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ION: 51, 127, 10N: 402, 405, 10N: 509, 512, 10N: 588, 609, INFORMATION:
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Carroll, Eddie 11..
Catino, Theodore Dwivedi, Poornima
Catino, Gary A.
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436,
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              289, 3
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GENERAL INFORMATION:
APPLICANT: Aglate, Paul A.
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.497
CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4027
; Sequence 7072, Application US/1065; Publication No. US20040229367A1; GENERAL INFORMATION:
APPLICANT: Randy M. Berka; APPLICANT: Michael W. Rey; APPLICANT: Jeffrey R.Shuster; APPLICANT: Sakari Kauppinen; APPLICANT: Ib Groth Clausen; APPLICANT: Peter Bjarke Olsen; TITLE OF INVENTION: Methods For Modern File Reference: 5849.200-US
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US-09-867-701-4027
; Sequence 4027, Application US/09867701
parent No. US20020132237A1
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US-10-653-047-7072
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NAME/KEY: misc_feature
LOCATION: (1)...(441)

OTHER INFORMATION: n = A
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                                                                 Monitoring
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PRIOR APPLICATION NUMBER: US/09/533,55

PRIOR FILING DATE: 2000-03-22

PRIOR APPLICATION NUMBER: 09/273,623

PRIOR FILING DATE: 1999-03-22

NUMBER OF SEQ ID NOS: 7860

SOFTWARE: FastSEQ for Windows Version

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10-653-047-7072
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Similarity 61.6%;
S; Conservative
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Kovalic, David
                                                                          GATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATTTGT
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TÁCGCGÁ
                        TACGCAA 190
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Cao, Yongwei
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larity 62.2%;
Conservative
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RESULT 10 US-09-960-352-6576

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SEQ ID NO 6576
LENGTH: 390
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Similarity 53.7%;
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AGGAGGCTGGAATTTG 182
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RMATION:
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Tao, Nengbing
Byatt, John C.
Mathialagan, N
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No. US20040265889A1
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Pred. No. 0.0002;
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RESULT 12
US-09-782-378A-21
; Sequence 21, App
; Patent No. US200
; GENERAL INFORMAT
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                                                                                                      TITLE OF INVENTION: Compositions and Metl
TITLE OF INVENTION: Modulators
FILE REFERENCE: 018501-000710US
CURRENT APPLICATION NUMBER: US/10/021,660
CURRENT FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: US/09/784,356
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: US 09/637,977
PRIOR FILING DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 135
SOFTWARE: FastSEQ for Windows Version 3.0
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Matches
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ORGANISM: Homo
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R: EOS Biotechnology, Inc.
INVENTION: No. US20030152926A1el Methods
INVENTION: Compositions and Methods of SINVENTION: Modulators
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Similarity 53.7%;
73; Conservative
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   Similarity
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OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
OF INVENTION: CANCER USING 140, 1470, 1686, 2089, 2427, 3702, 5891, 6428,
OF INVENTION: 7181, 7660, 25641, 69583, 49863, 8897, 1682, 17667, 9235,
OF INVENTION: 3703, 14171, 10359, 1660, 1450, 18894, 2088, 32427, 2160,
OF INVENTION: 9252, 9389, 1642, 85269, 10297, 1584, 9525, 14124, 4469,
OF INVENTION: 8990, 2100, 9288, 64698, 10480, 20893, 33230, 1586, 9943,
OF INVENTION: 16334, 68862, 9011, 14031, 6178, 21225, 1420, 32236, 2099,
OF INVENTION: 2150, 26583, 2784, 8941, 9811, 27444, 50566 OR 66428 MOLECULES
OF INVENTION NUMBER: US/10/354,358
NT APPLICATION NUMBER: US/10/354,358
NT FILING DATE: 2003-01-30
APPLICATION NUMBER: US 60/353,600
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G DATE: 2002-04-19
CATION NUMBER: US 60/382,995
G DATE: 2002-05-24
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APPLICANT: Dai, Hongyue
APPLICANT: He, Yudong
APPLICANT: Linsley, Peter
APPLICANT: Mao, Mao
APPLICANT: Roberts, Chris
APPLICANT: Van 't Veer, Laura
APPLICANT: Van de Vijver, Marc
APPLICANT: Van de Vijver, Marc
APPLICANT: Bernards, Rene
TITLE OF INVENTION: Diagnosis and Prognosis
FILE REFERENCE: 9301-175-99
CURRENT APPLICATION NUMBER: US/10/172,118
CURRENT FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: 60/380,770
PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 458
LENGTH: 1418
TYPE: DNA
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; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_000270
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## ALIGNMENTS

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1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60	ch 100.0%; Score 190; DB 7; Length 509;    Similarity 100.0%; Pred. No. 1.8e-50;   Similarity 100.0%; Pred. No. 1.8e-50;   Indels 0; Gaps 0;	9606" hbryonic s H7 and H EB" primed, fi ody outgro	Nat. Biotechnol. 22 (6), 707-716 (2004)  Contact: Brandenberger R  Regenerative Medicine  Geron Corporation 230 Constitution Drive, Menlo Park, CA 94025, USA  Tel: 650 473 8658  Fax: 650 473 7760  Email: rbrandenberger@geron.com Insert Length: 509	sapiens (human) sapiens sapiens yota; Metazoa; Chordata; Cra lia; Eutheria; Primates; Cat lia; Eutheria; Cat lenberger, R., Wei, H., Zhang, S. lenberger, R., Guegler, K. lenberger, R., Guegler, R. lenberger, R., Guegler, R	CN409509 509 bp mRNA linear EST 16-MAY-2004 17000423957987 GRN_EB Homo sapiens cDNA 5', mRNA sequence. CN409509 CN409509.1 GI:47396633

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Brandenberger,R., Wei,H., Zhang,5.,
Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalli,Y., Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalling, new Line, Lin
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17000600010132
CN409511
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Mammalia; E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: rbrandenberger@geron.com
Insert Length: 562 Std Error:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Geron Corporation
230 Constitution Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 650 473 8658
Fax: 650 473 7760
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                     TGTTACGCAA
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/db_xref="taxon:9606"
/tissue_type="embryonic s
                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="GRN_PREHEP"
/note="oligo dT_primed, full-length
from DMSO-treated hES cell line H9 |
feeder-free conditions"
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1 to 562)
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Sutheria; Primates;
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Pred. No. 1.9e-5
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Catarrhini; Hominidae;
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, Mandalam,R.
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                                                                                                                                                                                                                                                                                                                                                            562;
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BM839857
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Best Loc
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                                                                                                              280
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                                                                                                                                                                                                                                                              190;
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K-EST0116831 S13KMS5 Homo s
mRNA sequence.
BM839857
BM839857.1 GI:19196266
EST.
Homo sapiens (human)
                                                                                                                                                61
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Eukaryota;
Mammalia; E
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sapiens
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S Kim, N.S., na...
Oh, K.J., Cheong, J.L.
Kim, Y.S.
21C Frontier Korean EST Project 2...
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Fow: A column: 07
Tow: A column: 07
The stop: 580.
                       GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT
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,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
,Y.S.
                                                                                                                    AATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG
                                                                                                                                                                                                                                                                                          100.0%; Score 190; DB 4; larity 100.0%; Pred. No. 1.9e-50; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="S13KMS5"
/note="Vector: pCNS; Site_1: EcoRI; Site_2: NotI; The poly
(A) + RNA was dephosphorylated with bacterial alkaline
phosphatase (BAP) and then decapped with tabacco acid
pyrophosphatase (TAP). The decapped intact mRNA was
ligated with DNA-RNA linker including EcoR I site by
treatment of T4 RNA ligase and the first strand cDNA was
synthesized from oligo dT-selected mRNA by priming with
dT-tailed vector. The dT-tailed vector was adjusted to
have about 60nt. The cDNA vector was circularized with E.
coli DNA ligase after digestion of EcoRI which site is
also included in vector. An RNA strand converted to a DNA
strand by Okayama-Berg method. The obtained cDNA vectors
were used for transformation of competent cells E. coli
ToploF' by electroporation method. The cDNA libraries
constructed by this method are full-length enriched cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S13KMS5-31-A07"
/tissue_type="myeloma"
/cell_line="KMS-5"
/lab_host="Top10F'"
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Eukaryota; Metazoa; Cho
Mammalia; Eutheria; Pri
1 (bases 1 to 580)
Kim, N.S., Hahn, Y., Oh, J
Oh, K.J., Cheong, J.E., S
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BM840883
BM840883.1 GI
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Plate: 35 row: F column: 08
High quality sequence stop: 580.
Location/Qualifiers
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Tel: +82-42-860-4470
Fax: +82-42-860-4409
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K-EST0118036
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GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT
                                                                                                                                                                        100.0%;
larity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="Top10F'"
/clone lib="S13KMS5"
/clone lib="S13KMS5"
/note="Vector: pCNS; Site_1: EcoRI; Site_2: NotI; The poly
/note="Vector: pCNS; Site_1: EcoRI; Site_2: NotI; The pCNS; Site_1: NotI; Site_2: NotI; The pcNS; Site_2: 
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cell_line="KMS-5"
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/db_xref="taxon:9606"
/clone="S13KMS5-35-F08"
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Primates; Catarrhini;
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Pred. No. 1.9e-50;
Mismatches 0;
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, Daejeon 305-333, South Korea
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J.M., Park, H.S., Kim,
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Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation Nat. Biotechnol. 22 (6), 707-716 (2004)

Contact: Brandenberger R
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alia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Length: 638 Std Error:
Location/Qualifiers
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/clone_lib="GRN_EB"
/note="oligo dT_primed, full-length enriched cDNA library from embryoid body outgrowths derived from hES cell lines H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free conditions."
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1 (bases 1 to 738)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, M

Unpublished (1999)

Contact: Robert Strausberg, Ph.C

Email: cgapbs-r@mail.nih.gov
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                             aomo sapiens MTAP gene, VIRTUAL TI
genomic survey sequence.
AY405891
AY405891.1 GI:397616
GSS.
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gene trios
Science 302 (5652), 1960-1963 (2003)
14671302
2 (bases 1 to 813)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sladams, M.D. and Cargill, M.
Direct Submission
                                                                                                                                                             Homo bapium.
Eukaryota; Metazoa; Chordaud, ——
Eukaryota; Metazoa; Chordaud, ——
Mammalia; Eutheria; Primates; Catarrhini; Hominium.

1 (bases 1 to 813)
1 (bases 1 to 813)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, J.
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Todd, M.A., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lebkowski, J and Stanton, L.W.
Transcriptome characterization elucidates signaling control human ES cell growth and differentiation Nat. Biotechnol. 22 (6), 707-716 (2004)
Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
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Eukaı
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rring nonneutral evolution from human-chimp-mouse
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larity 100.0%;
Conservative 0
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Length: 751 Std Error:
Location/Qualifiers
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/note="oligo dT_primed, full-length enriched cDNA library
from DMSO-treated hES cell line H9 (p22) maintained in
feeder-free conditions"
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xref="taxon:9606"
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                                                                                                                                                                                                                                                                       Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 2e-50;
Mismatches
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                                                      Thomas, P., Kejariwal, A., 
l., Lu, F., Murphy, B.,
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                                       Sninsky,
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BM903599
LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
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5', mRNA sequence.
BM903599
BM903599.1 GI:19352956
EST.
Homo sapiens (human)
Homo sarian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19
                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12707 row: f column: 17
                                                                                                                                                                                                                                                                                                  1 (bases 1 to 1037)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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This sequence was made by sequencing genomic them based on alignment.
Location/Qualifiers
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                    sapiens
                                         /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5722000"
/lab_host="DH10B"
/clone_lib="NIH_MGC_125"
/note="Organ: ovary (pool of 3); Vector: pCMV
Site 1: EcoRV (destroyed); Site 2: NotI; RNA of
three ovaries, from females ranging in age
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'gene="MTAP"
'locus_tag="HCM2375"
                                                                                                              organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                           Metazoa; Chordata;
Sutheria; Primates;
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BM925551
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E 1 (bases 1 to 1047)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM12816 row: b column: 06
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quality sequence stop:
Location/Qualifiers
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sapiens
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                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5763749"
/lab_host="DH108"
/clone_lib="NIH_MGC_114"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source anonymous pool of
male_brains, age range 23-27 yo. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroye
upon cloning). Average insert size 1.5 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 019. Not
this is a NIH_MGC Library."
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6710137 NIH_MGC_114 Homo
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BX459089
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Best Local S
Matches 190
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Best Local Similarity 100.0%;
Matches 190; Conservative 0
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BX459089
5-PRIME,
BX459089
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Mammalia; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)
On May 22, 2003 this sequence version replace Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       division of Invitrogen.
This sequence belongs to sequence cluster 5445.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSODEO12CDO1QP1&c=5445.f
Location/Qualifiers
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EST.
                                                                       1 100.0%;
Similarity 100.0%;
90; Conservative 0
GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC
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                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DE012YH01"
/tissue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT_6; 1st strand cDNA was primed/
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned :
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
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1 to 1064)
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Eutheria; Primates;
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Pred. No. 2.2e-50;
Mismatches 0;
                                                                   Score 190; DB 5;
Pred. No. 2.2e-50;
Mismatches 0;
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and clone into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster For more information about the constructed by the sequence cluster for more information about the constructed belongs to sequence cluster for more information about the constructed belongs to sequence cluster for more information about the constructed belongs to sequence cluster for more information about the constructed belongs to sequence cluster for more information about the constructed belongs to sequence cluster for more information about the constructed by the constructed belongs to sequence cluster for more information about the constructed by the constructed
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AL543068
AL543068.3 GI:45718631
EST.
Homo sapiens (human)
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On Feb 15, 2001 this sequence version replace Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
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1 (bases 1 to 1075)
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                                                                                                                                                                                                                                                                                      100.0%; Score 190; DB 1; larity 100.0%; Pred. No. 2.2e-50; Conservative 0; Mismatches 0;
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sapiens
                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DI002YH04"

/tissue_type="PLACENTA COT 25-NORMALIZED"

/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR \
sites of the pCMVSPORT 6 vector. Library was normalized.
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8 1 (bases 1 to 1380)

8 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

L Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
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12477932
2 (bases 1 to 1380)
Strausberg, R.
Direct Submission
Submitted (09-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
                                                                                                                                Clone distribution:
through the I.M.A.G.
Series: IRAL Plate:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC Project URL: http://i
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo
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Eutheria;
was selected for full length sequencing because following selection criteria: matched mRNA gi: has the following problem: frame shifted.
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Primates;
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Consortium/LLNL at:
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Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NA Library Preparation: Life Technologies, Inc.
NA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
NA Sequencing by: Agencourt Bioscience Corporation
NA Sequencing by: Agencourt Bioscience
NA Sequencing by: Agencourt Bioscience
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          act: Robert Strausberg, Ph.D.
l: cgapbs-r@mail.nih.gov
sue Procurement: ATCC
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COURT_6417999 NIH_MGC_71 Homo sapiens cDNA clone
mRNA sequence.
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/db_xref="taxon:9606"
/clone="IMAGE:3546198"
/tissue_type="Placenta, of the content of the con
                               /tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_71"
/clone_lib="NIH_MGC_71"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_Site_2: Sall; Cloned unidirectionally. Primer:
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'db_xref="taxon:9606"
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Pred. No. 2.4e-50;
Mismatches 0;
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  Match
                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1479 row: 1 column: 10
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Mammalia; Eutheria;
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Location/Qualifiers
                                                                                                                                /organism="Homo sapiens"
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4668825"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_60"
/clone_lib="NIH_MGC_60"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);
Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI
(ggccattatggcc); Double-stranded cDNA was prepared from
(ggccattatggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as
                                       follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.5 kb (range 0.9-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
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Pred. No. 4.5e-50;
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Catarrhini;
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i; Hominidae;
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